

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:25:16 ; Search time 7.60425 Seconds
(without alignments)
661.194 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110
Perfect score: 78
Sequence: 1 AYGWQDIYSL 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	478	2 AAR46065	Aar46065 Mutant al
2	78	100.0	478	2 AAR72450	Aar72450 Aspergill
3	78	100.0	478	2 AAR78270	Aar78270 Aspergill
4	78	100.0	478	2 AAW14500	Aaw14500 Aspergill
5	78	100.0	498	4 AAB84206	Aab84206 Amino aci
6	78	100.0	498	8 ADT89632	Adt89632 Aspergill
7	78	100.0	499	8 ADT89628	Adt89628 Aspergill
8	78	100.0	1095	6 ABP96630	Abp96630 Alpha-amy
9	75	96.2	495	6 ABB80177	Abb80177 A. fumiga
10	70	89.7	423	4 ABB09072	Abb09072 Aspergill
11	70	89.7	494	6 ABP97894	Abp97894 Amino aci
12	69	88.5	55	2 AAR88213	Aar88213 Alpha-amy
13	69	88.5	493	2 AAR88212	Aar88212 Alpha-amy
14	69	88.5	500	8 ADS23436	Adn23436 Bacterial
15	67	85.9	513	8 ADN19570	Adn19570 Bacterial
16	65	83.3	547	6 ABB80179	Abb80179 A. fumiga
17	64	82.1	484	5 AAE24207	Aae24207 Aspergill
18	64	82.1	484	8 ADS75939	Ads75939 Aspergill
19	63	80.8	555	6 ABP97896	Abp97896 Amino aci
20	63	80.8	567	6 ABP97899	Abp97899 Amino aci
21	62	79.5	478	2 AAR79025	Aar79025 Mature ta
22	58	74.4	468	2 AAR24136	Aar24136 Alpha-amy
23	58	74.4	494	1 AAP70571	Aap70571 Alpha-amy
24	58	74.4	630	6 ABB80178	Abb80178 A. fumiga
25	57	73.1	549	6 ABP97895	Abp97895 Amino aci

26	56	71.8	493	8 ADS44293	Ads44293 Bacterial
27	54	69.2	468	2 AAR63184	Aar63184 Variant a
28	53	67.9	468	2 AAR63185	Aar63185 Variant a
29	53	67.9	564	8 ADS44249	Ads44249 Bacterial
30	52	66.7	711	5 ADP26024	Adp26024 Streptoco
31	50	64.1	452	2 AAR63186	Aar63186 Variant a
32	50	64.1	511	1 AAP81161	Aap81161 Recombina
33	50	64.1	511	1 AAP81180	Aap81180 Sequence
34	50	64.1	512	2 AAR07574	Aar07574 Alpha-amy
35	49	62.8	468	2 AAR63187	Aar63187 Variant a
36	49	62.8	656	2 AAR06109	Aar06109 Sequence
37	49	62.8	686	1 AAP61518	Aap61518 Sequence
38	49	62.8	686	2 AAW17605	Aaw17605 Bacillus
39	49	62.8	686	2 AAW17600	Aaw17600 Bacillus
40	49	62.8	686	2 AAW17603	Aaw17603 Bacillus
41	49	62.8	686	2 AAW17592	Aaw17592 Bacillus
42	49	62.8	686	2 AAW17596	Aaw17596 Bacillus
43	49	62.8	686	2 AAW06773	Aaw06773 Wild type
44	49	62.8	686	2 AAW17599	Aaw17599 Bacillus
45	49	62.8	686	2 AAW17594	Aaw17594 Bacillus

ALIGNMENTS

RESULT 1

AAR46065
ID AAR46065 standard; protein; 478 AA.
XX
AC AAR46065;
XX
DT 25-MAR-2003 (revised)
DT 18-JUL-1994 (first entry)
XX
DE Mutant alpha-amyase.
XX
KW Methionine substitution; stability; activity; detergent;
KW dishwashing agents; liquefaction agents.
XX
OS Aspergillus oryzae.
XX
PN WO9402597-A1.
XX
PD 03-FEB-1994.
XX
PF 06-JUL-1993; 93WO-DK000230.
XX
PR 23-JUL-1992; 92DK-00000946.
PR 16-DEC-1992; 92DK-00001503.
PR 15-MAR-1993; 93DK-00000292.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Svendsen A, Bisgaard-Frantzen H;
XX
WP 1994-048855/06.
XX
Mutant alpha-amyase from Bacillus species comprising a methionine substitution - with improved stability and activity at low pH, for use in detergents, dishwashing agents and liquefaction agents.
PS Claim 1; Page 7; 20pp; English.
XX
The sequence os that of the Aspergillus oryzae alpha amylase, sold commercially as FUNGAMYL (TM) by Novo Nordisk A/S. The sequence can be mutated by substitution of one or more of its methionine residues for any amino acid other than cysteine. The mutant alpha-amyase exhibits a better activity level and better stability in the presence of oxidising agents than previous mutant alpha amylases, and improved thermostability at moderately low pH. The enzyme can be used as an additive for detergents, dishwashing agents and liquefaction agents. (Updated on 25-MAR-2003 to correct PN field.)
XX

RESULT 3
AAR78270
ID AAR

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FH Key Location/Qualifiers
FT 13..45 /label= loop 1 modification region
FT Misc-difference /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 7-23 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 33"
FT 14..40 /label= loop 1 modification region
FT Misc-difference /note= "at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 8-18 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 35"
FT 28..42 /label= loop 1 modification region
FT Misc-difference /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 12-19 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 30"
FT 32..38 /label= loop 1 modification region
FT Misc-difference /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 14-15 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 32"
FT 66..84 /label= loop 2 modification region
FT Misc-difference /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 44-57 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 18"
FT 70..78 /label= loop 2 modification region
FT Misc-difference /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 48-51 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 20"
FT 98..210 /label= loop 3 modification region
FT Misc-difference /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 117-185 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 24"
FT 102..206 /label= loop 3 modification region
FT Misc-difference /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 121-181 of AAW14499 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 26"
FT 121..181 /label= loop 3 modification region
FT Misc-difference /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to this fragment is deleted or replaced with a fragment
FT corresponding to 102-206 of AAW14499; claim 41"
FT 121..174 /label= loop 3 modification region
FT Misc-difference /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to this fragment is deleted or
FT replaced with a fragment corresponding to 102-199 of
FT AAW14499; claim 42"
FT 165..177 /label= loop 3 modification region
FT Misc-difference /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 195-202 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 21"
FT 166..173 /label= loop 3 modification region
FT Misc-difference /note= "preferred region where at least one amino acid

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FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 196-198 of AAW14499 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 23"
FT 181..184 /note= "an amino acid fragment corresponding to this
FT region is deleted from the parent sequence of a variant
FT Fungamyl; claim 43"
FT 291..313 /label= loop 8 modification region
FT Misc-difference /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 322-346 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 36"
FT 297..313 /label= loop 8 modification region
FT Misc-difference /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 325-345 of AAW14499 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 38"
FT WO9623874-A1.
XX
XX 08-AUG-1996.
XX
XX 05-FEB-1996; 96WO-DK0000057.
XX
XX 03-FEB-1995; 95DK-00000128.
XX 23-OCT-1995; 95DK-00001192.
XX 10-NOV-1995; 95DK-00001256.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Svendsen A, Bisgard-Frantzen H, Borchert TV;
XX WPI; 1996-371424/37.
XX
XX Alpha-amylase variants and methods of production - have altered
XX properties such as calcium dependency, substrate binding and stability.
XX
XX Disclosure; Page 87-88; 171pp; English.
XX
XX The present sequence is the mature Aspergillus oryzae alpha-amylase (A).
XX Variants of parent tetramyl- and fungamyl-like alpha-amylases (and
XX methods of constructing them) are claimed. Examples of variants are
XX featured above. The variants have altered properties such as calcium
XX dependency, substrate binding and stability. Also one or more proline or
XX cysteine residues in the variant is modified or replaced with a non-
XX proline or non-cysteine residue such as alanine. The variants can be used
XX for (dish)washing, as detergent additives or for fabric desizing or
XX starch liquefaction. They can also be used for the production of
XX sweeteners and ethanol from starch. See also AAW14498-99
XX
XX Sequence 478 AA;
SQ
Query Match 100.0%; Score 78; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AYHGYWQDIYSL 13
DB 78 AYHGYWQDIYSL 90
RESULT 5
AAB84206
ID AAB84206 standard; protein; 498 AA.
XX
XX AAB84206;
XX
XX 06-AUG-2001 (first entry)
XX

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XX The present invention relates to a method of producing heterologous
CC biological substance. The method involves culturing mutant of wild-type
CC *Aspergillus niger* strain in medium suitable for producing heterologous
CC biological substance, where mutant strain comprises first nucleotide
CC sequence encoding heterologous biological substance and second nucleotide
CC sequences comprising modification of glucoamylase (glua) and recovering
CC heterologous biological substance. The present sequence is the
CC *Aspergillus niger* neutral alpha-amylase B (amyB) protein.
XX
SQ Sequence 499 AA;

Query Match 100.0%; Score 78; DB 8; Length 499;
Best Local Similarity 100.0%; Pred. NO. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
Db 99 AYHGYWQDIYSL 111
|||||
RESULT 8
ABP96630
ID ABP96630 standard; protein; 1095 AA.
XX
AC ABP96630;
XX
DT 02-JUN-2003 (first entry)
DE Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45.
XX
KW Self-processing plant; plant; processing enzyme; alpha-amylase; grain;
KW pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase;
KW mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch;
KW maltodextrin; ethanol; fermentation; beverage; enzyme.
XX
OS *Aspergillus shirousami*.
OS Synthetic.
XX
PN WO2003018766-A2.
XX
PD 06-MAR-2003.
XX
PF 27-AUG-2002; 2002WO-US027129.
XX
PR 27-AUG-2001; 2001US-0315281P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Lanahan MB, Basu SS, Batie CJ, Chen W, Craig J, Kinkema M;
XX
DR WPI; 2003-268420/26.
DR N-PSDB; ACC44572.
XX
PT Novel polynucleotide encoding hyperthermophilic processing enzymes e.g.
PT alpha-amylase, useful for producing plant to produce food products having
PT improved taste or fermentable substrates for ethanol.
XX
PS Claim 1; Page 107; 158pp; English.
XX
CC The present invention describes polynucleotides which encode processing
CC enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose
CC isomerase, or glucoamylase) that are optimised for expression in plants.
CC The polynucleotides encode mesophilic, thermophilic or hyperthermophilic
CC processing enzymes, which are activated under suitable conditions to act
CC upon the desired substrate. Also described are self-processing transgenic
CC plants and plant parts, e.g. grain, which express one or more of these
CC enzymes and have an altered composition that facilitates plant and grain
CC processing. Also described is a method (M) for converting starch to
CC starch-derived products in a transformed plant part (TPP), by activating
CC the starch processing enzyme contained in it. Transgenic grain is useful
CC for preparing maltodextrin. A transformed plant (TP) can be used to
CC produce food products having improved taste and to produce fermentable

CC substrates for ethanol and fermented beverages. (M) eliminates the need
CC to mill or physically disrupt the integrity of plant parts prior to
CC recovery of starch-derived products. The present sequence represents
CC alpha-amylase/glucoamylase fusion protein, which is given in the
CC exemplification of the present invention
XX
SQ Sequence 1095 AA;

Query Match 100.0%; Score 78; DB 6; Length 1095;
Best Local Similarity 100.0%; Pred. NO. 0.0025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
Db 78 AYHGYWQDIYSL 90
|||||
RESULT 9
ABB80177
ID ABB80177 standard; protein; 495 AA.
XX
AC ABB80177;
XX
DT 11-AUG-2003 (first entry)
DE A. fumigatus AFAAL1.
XX
KW Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
KW beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
KW polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
KW glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
KW glyceride; starch; maltodextrin; oxidated phenolic compound;
KW polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
KW textile; tea liquor; cleaning ability.
XX
OS *Aspergillus fumigatus*.
XX
PN WO2003012071-A2.
XX
PD 13-FEB-2003.
XX
PF 05-AUG-2002; 2002WO-US024842.
XX
PR 03-AUG-2001; 2001US-0309870P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Jiang B, Storms R, Roemer T, Bussey H;
XX
DR WPI; 2003-332729/31.
DR N-PSDB; ABQ80345, ABQ80346.
XX
PT Novel isolated *Aspergillus fumigatus* polypeptide, useful in various
PT industries such as those involved in the making of food and feed,
PT beverages, textiles and detergents.
XX
PS Claim 17; Page 134-35; 169pp; English.
XX
CC The sequences given in ABB80164-87 show enzymatic proteins derived from
CC A. fumigatus. These proteins display the catalytic activity of an enzyme
CC such as tannase, cellulase, glucose oxidase, glucoamylase, phytase, beta-
CC galactosidase, invertase, lipase, alpha-amylase, laccase,
CC polygalacturonase or xylanase. Compositions comprising the tannase are
CC useful for modulating the amount of compounds that comprise a gallate
CC ester linkage in a composition. Compositions comprising cellulase are
CC useful for modulating the amount of cellulose in a composition.
CC Compositions comprising glucose oxidase are useful for modulating the
CC amount of glucose or oxygen in a composition. Compositions comprising
CC phytase are useful for modulating the amount of myo-inositol phosphates
CC in a composition. Compositions comprising beta-galactosidase are useful
CC for modulating the amount of lactose in a composition. Compositions
CC comprising sucrose or invertase are useful for modulating the amount of
CC sucrose in a composition. Compositions comprising lipase are useful for

modulating the amount of glyceride in a composition. Compositions comprising alpha-amylases are useful for modulating the amount of starches or maltodextrins in a composition. Compositions comprising lactase are useful for modulating the amount of oxidized phenolic compounds in a composition. Compositions comprising polygalacturonases are useful for modulating the amount of high or low molecular weight polygalacturonic acid chains in a composition. Compositions comprising xylanases are useful for modulating the amount of xylan or xylo-oligomers in a composition. The A. fumigatus proteins and corresponding DNA's are useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents. The DNA's are useful to express recombinant enzymes for characterization, modification or industrial uses, to compare with the nucleotide sequence of A. fumigatus to identify duplicated genes of paralogs having the same or similar biochemical activity and/or function, to compare with nucleic acid sequence of other related or distant fungal organisms to identify potential orthologous enzyme genes for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, and to raise anti-protein antibodies. The polypeptide having tannase activity increases the yield of tea liquor from tea leaves, improves the colour, flavour and health benefits of tea products, particularly an instant tea product. The polypeptide having cellulase activity enhances cleaning ability of detergent compositions

XX SQ Sequence 495 AA;

Query Match 96.2%; Score 75; DB 6; Length 495;
Best Local Similarity 92.3%; Pred. No. 0.0032;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVHGYWQDIYSL 13
| | | | | | | | | |
Db 97 AVHGYWQDIYSV 109

RESULT 10
ID ABB09072 standard; protein; 423 AA.
XX AC ABB09072;
XX DT 26-JUN-2002 (first entry)
XX DE Aspergillus oryzae TAKA protein (TAA).
XX KW Thermus sp. IM6501; maltogenic amylase; EC 3.2.1.133; crystallisation;
XX KM protein co-ordinate data; 3 dimensional structure.
XX OS Aspergillus oryzae.
XX PN KR2001027418-A.
XX PD 06-APR-2001.
XX PF 09-SEP-1999; 99KR-00039130.
XX PR 09-SEP-1999; 99KR-00039130.
XX PA (POST-) POSTECH FOUND.
XX PI (SAMY-) SAMYANG GENEX CORP.
XX PT Kim TJ, Park GH;
XX WP; 2001-534477/59.
XX DR Manufacturing maltogenic amylase having improved transglycosylation
XX PT activity, comprises using crystallization.
XX PS Disclosure; Page 188; 196pp; Korean.
XX CC The present invention describes manufacturing maltogenic amylase (EC
XX CC 3.2.1.133) having improved transglycosylation activity, comprising using
XX CC crystallisation and the three dimensional structure of maltogenic

CC amylase. Manufacturing maltogenic amylase comprises the following steps:
CC (i) obtaining a gene of maltogenic amylase from Thermus sp. IM6501 (KCTC
CC 5027BP) and inserting the gene into plasmid pUC119 to construct
CC recombinant DNA (pThMAL19); (ii) inserting the recombinant DNA to
CC Escherichia coli MC1061, which is cultivated at 37 plus degrees Celsius
CC for 10 hours in Luria-Bertani (LB) media and centrifuging the media to
CC obtain a microbial cell; (iii) suspending the microbial cell with buffer
CC solution at pH 7.5 and obtaining supernatant; and (iv) passing the
CC supernatant through column chromatography and obtaining purified
CC maltogenic amylase. The maltogenic amylase is a dimer comprised of two
CC maltogenic amylase molecules, and a Thermus sp. IM6501 maltogenic amylase
CC (ThMA) crystal. The amylase has a structure containing an activated
CC region that consists of amino acid residues of Asp-328, Glu-357, Asp-424,
CC and a pocket with glucose bound that consists of amino acid residues of
CC Pro44, Tyr45, Arg81, Arg83, Prol18, Cys116, Asn133, Glu132, Val132,
CC and His1360. The present sequence represents Aspergillus oryzae TAKA
CC protein (TAA), given in comparison with ThMA in the present invention
XX
SQ Sequence 423 AA;

Query Match 89.7%; Score 70; DB 4; Length 423;
Best Local Similarity 92.3%; Pred. No. 0.016;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVHGYWQDIYSL 13
| | | | | | | | | |
Db 74 AMHGYWQDIYSL 86

RESULT 11
ABP97894
ID ABP97894 standard; protein; 494 AA.
XX AC ABP97894;
XX DT 17-JUN-2003 (first entry)
XX DE Amino acid sequence of an alpha-amylase of Aspergillus niger.
XX KW Alpha-amylase; enzyme; endohydrolysis; 1,4-alpha-glucosidic linkage;
XX KM oligosaccharide; polysaccharide; baking.
XX OS Aspergillus niger.
XX PN WO2003016535-A2.
XX PD 27-FEB-2003.
XX PF 02-AUG-2002; 2002WO-NL000522.
XX PR 16-AUG-2001; 2001EP-00000379.
XX PR 16-AUG-2001; 2001EP-00000380.
XX PR 16-AUG-2001; 2001EP-00000381.
XX PR 16-AUG-2001; 2001EP-00000382.
XX PR 16-AUG-2001; 2001EP-00000383.
XX PR 16-AUG-2001; 2001EP-00000384.
XX PA (STAM) DSM NV.
XX PI Maier D, Stock A, Wagner C, Folkers U, Albermann K, Hopper S;
XX WP; 2003-312758/30.
XX DR New polynucleotide from a filamentous fungus, preferably Aspergillus
XX PT niger, useful in a baking process.
XX PS Claim 13; Page 61-63; 81pp; English.
XX CC The present sequence is an alpha-amylase enzyme of the filamentous fungus
XX CC Aspergillus niger. Alpha-amylases catalyse the endohydrolysis of 1,4-
XX CC alpha-glucosidic linkages in oligosaccharides and polysaccharides. The
XX CC alpha-amylase polynucleotides and polypeptides of the invention are
XX CC useful in a baking process

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XX SQ Sequence 494 AA;
Query Match      89.7%; Score 70; DB 6; Length 494;
Best Local Similarity 84.6%; Pred. No. 0.019;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
DB 94 AYHGYWQDDIYSL 106

RESULT 12
AAR88213
ID AAR88213 standard; peptide; 55 AA.
XX
AC AAR88213;
XX
DT 16-OCT-2003 (revised)
DT 03-APR-1996 (first entry)
XX
DE Alpha-amylase fragment.
XX
KW Alpha-amylase; thermostable enzyme; baking; Thermomyces lanuginosus; PCR;
KW polymerase chain reaction.
XX
OS Thermomyces lanuginosus; CBS 223.63.
XX
PN WO9601323-A1.
XX
PD 18-JAN-1996.
XX
PF 03-JUL-1995; 95WO-EP002607.
XX
PR 04-JUL-1994; 94GB-00013419.
XX
PA (DANI-) DANISCO AS.
XX
PI Michelsen B, Rasmussen P;
XX
DR WPI; 1996-087673/09.
XX
N-PSDB; AAT10562.
XX
PT Thermophilic alpha-amylase with activity range of 60-80 degrees C -
PT derived from Thermomyces lanuginosus, useful in the prepn. of foodstuffs
PT and bakery prods. esp. bread.
XX
PS Disclosure; Page 40; 94pp; English.
XX
CC Fragments (AAR88213-14) of Thermomyces lanuginosus thermostable alpha-
CC amylase (AAR88212) are the products of DNA fragments (AAT10565-66)
CC generated from T. lanuginosus genomic DNA by PCR using primers based on
CC conserved regions of alpha-amylase genes. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 55 AA;
Query Match      88.5%; Score 69; DB 2; Length 55;
Best Local Similarity 76.9%; Pred. No. 0.0027;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
DB 26 SYHGYWQDDIYSL 38

RESULT 13
AAR88212
ID AAR88212 standard; protein; 493 AA.
XX
AC AAR88212;
XX
DT 16-OCT-2003 (revised)
XX
DT 03-APR-1996 (first entry)
XX
DE Alpha-amylase.
XX
KW Alpha-amylase; thermostable enzyme; baking; Aspergillus niger.
XX
OS Thermomyces lanuginosus; CBS 224.63.
XX
PN WO9601323-A1.
XX
PD 18-JAN-1996.
XX
PF 03-JUL-1995; 95WO-EP002607.
XX
PR 04-JUL-1994; 94GB-00013419.
XX
PA (DANI-) DANISCO AS.
XX
PI Michelsen B, Rasmussen P;
XX
DR WPI; 1996-087673/09.
XX
N-PSDB; AAT10562.
XX
PT Thermophilic alpha-amylase with activity range of 60-80 degrees C -
PT derived from Thermomyces lanuginosus, useful in the prepn. of foodstuffs
PT and bakery prods. esp. bread.
XX
PS Claim 3; Page 36-38; 94pp; English.
XX
CC A thermostable alpha-amylase (AAR88212) of Thermomyces lanuginosus CBS
CC 224.63 is expressed in Aspergillus niger hosts using a gene (AAT10562)
CC isolated from a T. lanuginosus gene library. The recombinant enzyme (54-
CC 60 kDa) shows optimal activity at 60-70 deg and pH 5.8-6, has a pI of 3.7
CC and is active at 60-80 deg. (Updated on 16-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 493 AA;
Query Match      88.5%; Score 69; DB 2; Length 493;
Best Local Similarity 76.9%; Pred. No. 0.027;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
DB 98 SYHGYWQDDIYSL 110

RESULT 14
ADS23436
ID ADS23436 standard; protein; 500 AA.
XX
AC ADS23436;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #12469.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX

```

PD	18-DEC-2003.	
XX		
PF	20-FEB-2003; 2003US-00369493.	
XX		
PN	21-FEB-2002; 2002US-0360039P.	
XX		
PA	(CAOY/) CAO Y.	
PA	(HINK/) HINKLE G J.	
PA	(SLAT/) SLATER S C.	
PA	(CHEN/) CHEN X.	
PA	(GOLD/) GOLDMAN B S.	
XX		
PI	Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;	
XX		
DR	WPI; 2004-061375/06.	
XX		
PT	New recombinant DNA construct comprising a promoter positioned to provide	
PT	for expression of a polynucleotide encoding a polypeptide from a	
PT	microbial source, useful for producing plants with improved properties.	
XX		
PS	Claim 1; SEQ ID NO 12469; 122pp; English.	
XX		
CC	The invention relates to a recombinant DNA construct comprising a	
CC	promoter functional in a plant cell, where the promoter is positioned to	
CC	provide for expression of a polynucleotide encoding a polypeptide from a	
CC	microbial source. The invention also relates to a transformed plant	
CC	comprising the recombinant DNA construct and a method of producing a	
CC	transformed plant having an improved property. The plant is a crop plant	
CC	such as maize or soybean. The method of producing a transformed plant	
CC	having an improved property comprises transforming a plant with the	
CC	recombinant DNA construct and growing the transformed plant with the	
CC	polynucleotide or polypeptide is useful for improving plant properties.	
CC	improved plant properties, e.g. improved cold, heat or drought tolerance,	
CC	tolerance to herbicides, extreme osmotic conditions, pathogens or pests,	
CC	of the cell cycle pathway with plant growth regulators, increased rate of	
CC	homologous recombination, modified seed oil or protein yield and/or	
CC	content, improved yield by modification of carbohydrate, nitrogen or	
CC	phosphorus use and/or uptake, by modification of photosynthesis or by	
CC	providing improved plant growth and development under at least one stress	
CC	condition. This sequence represents a bacterial polypeptide used in the	
CC	scope of the invention. Note: The sequence data for this patent did not	
CC	form part of the printed specification but was obtained in electronic	
CC	format from USPTO at seqdata.uspto.gov/sequence.html.	
XX		
XX	Sequence 500 AA;	
Qy	Query Match 88.5%; Score 69; DB 8; Length 500;	
Db	Best Local Similarity 84.6%; Pred. No. 0.027;	
	Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
	1 AYHGYYQDDIYSL 13	
	82 AYHGYWQDDMYSL 94	
RESULT 15		
ADN19570	ADN19570 standard; protein; 513 AA.	
XX		
AC	ADN19570;	
XX		
DT	02-DEC-2004 (first entry)	
XX		
DE	Bacterial polypeptide #2223.	
XX		
KW	Recombinant DNA construct; transformed plant; improved plant property;	
KW	cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;	
KW	pathogen tolerance; pest tolerance; plant disease resistance;	
KW	cell cycle pathway modification; plant growth regulator;	
KW	homologous recombination; seed oil yield; protein yield; carbohydrate;	

KW	nitrogen; phosphorus; photosynthesis; lignin; galactomannan;	
KW	bacterial polypeptide.	
XX		
OS	Bacteria.	
XX		
PN	US2003233675-A1.	
XX		
PD	18-DEC-2003.	
XX		
PF	20-FEB-2003; 2003US-00369493.	
XX		
PR	21-FEB-2002; 2002US-0360039P.	
XX		
PA	(CAOY/) CAO Y.	
PA	(HINK/) HINKLE G J.	
PA	(SLAT/) SLATER S C.	
PA	(CHEN/) CHEN X.	
PA	(GOLD/) GOLDMAN B S.	
XX		
PI	Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;	
XX		
DR	WPI; 2004-061375/06.	
XX		
PT	New recombinant DNA construct comprising a promoter positioned to provide	
PT	for expression of a polynucleotide encoding a polypeptide from a	
PT	microbial source, useful for producing plants with improved properties.	
XX		
PS	Claim 1; SEQ ID NO 2223; 122pp; English.	
XX		
CC	The invention relates to a recombinant DNA construct comprising a	
CC	promoter functional in a plant cell, where the promoter is positioned to	
CC	provide for expression of a polynucleotide encoding a polypeptide from a	
CC	microbial source. The invention also relates to a transformed plant	
CC	comprising the recombinant DNA construct and a method of producing a	
CC	transformed plant having an improved property. The plant is a crop plant	
CC	such as maize or soybean. The method of producing a transformed plant	
CC	having an improved property comprises transforming a plant with the	
CC	recombinant DNA construct and growing the transformed plant, where the	
CC	polynucleotide or polypeptide is useful for improving plant properties.	
CC	The recombinant DNA construct is useful for producing plants with	
CC	improved plant properties, e.g. improved cold, heat or drought tolerance,	
CC	tolerance to herbicides, extreme osmotic conditions, pathogens or pests,	
CC	increased resistance to plant disease, better growth rate by modification	
CC	of the cell cycle pathway with plant growth regulators, increased rate of	
CC	homologous recombination, modified seed oil or protein yield and/or	
CC	content, improved yield by modification of carbohydrate, nitrogen or	
CC	phosphorus use and/or uptake, by modification of photosynthesis or by	
CC	providing improved plant growth and development under at least one stress	
CC	condition. This sequence represents a bacterial polypeptide used in the	
CC	scope of the invention. Note: The sequence data for this patent did not	
CC	form part of the printed specification but was obtained in electronic	
CC	format from USPTO at seqdata.uspto.gov/sequence.html.	
XX		
XX	Sequence 513 AA;	
Qy	Query Match 85.9%; Score 67; DB 8; Length 513;	
Db	Best Local Similarity 76.9%; Pred. No. 0.057;	
	Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	
	1 AYHGYWQDDIYSL 13	
	100 AYHGYWQDDIYTL 112	
Search completed:	November 7, 2005, 18:57:40	
Job time :	8.60425 secs	

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:40:32 ; Search time 0.810811 Seconds
(Without alignments)
830.671 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167

Perfect score: 40

Sequence: 1 SSQDYFH 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79:*

2: PIR1:*

3: PIR2:*

4: PIR3:*

5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	478	2 JK0201	alpha-amylase (EC 3.2.1.1)
2	40	100.0	498	2 A48305	alpha-amylase (EC 3.2.1.1)
3	40	100.0	499	1 ALAS1	alpha-amylase (EC 3.2.1.1)
4	40	100.0	499	1 ALAS3	alpha-amylase (EC 3.2.1.1)
5	40	100.0	499	2 JS0663	alpha-amylase (EC 3.2.1.1)
6	40	100.0	499	2 JT0466	alpha-amylase (EC 3.2.1.1)
7	40	100.0	499	2 JN0588	alpha-amylase (EC 3.2.1.1)
8	40	100.0	499	2 B48305	alpha-amylase (EC 3.2.1.1)
9	40	100.0	624	1 JC4510	pullulanase (EC 3.2.1.1)
10	34	85.0	130	2 H71415	hypothetical prote
11	33	82.5	420	2 T42616	envelope protein -
12	33	82.5	601	2 T18787	hypothetical prote
13	33	82.5	1131	2 T41943	major DNA binding
14	33	82.5	4351	2 T00252	MEGF1 protein - ra
15	32	80.0	144	2 JC7121	androgenic gland h
16	32	80.0	180	2 B95039	hypothetical prote
17	32	80.0	289	2 A43562	homeotic protein H
18	32	80.0	317	2 E84088	restriction endonu
19	32	80.0	351	2 E86187	YUP8H12.10 [impor
20	32	80.0	419	2 S61245	probable virion gl
21	32	80.0	419	2 T15199	hypothetical prote
22	32	80.0	482	2 A90248	conserved hypothet
23	32	80.0	685	2 S67146	probable membrane
24	32	80.0	820	1 DEECK	thra bifunctional
25	32	80.0	820	2 B85480	aspartokinase I, h
26	32	80.0	820	2 B90629	aspartokinase I, h
27	32	80.0	820	2 AC0502	aspartokinase I/ho
28	31	77.5	67	2 T17658	hypothetical prote
29	31	77.5	104	2 S49803	hypothetical prote

30	31	77.5	214	2 B75513	pyridoxamine 5-pho
31	31	77.5	261	2 AF1307	hypothetical prote
32	31	77.5	261	2 AF1679	hypothetical prote
33	31	77.5	386	2 S72435	RNA-binding protei
34	31	77.5	461	2 F86597	UDP-glucose pyroph
35	31	77.5	461	2 H72024	UDP-N-acetylglucos
36	31	77.5	597	2 T35746	hypothetical prote
37	31	77.5	614	1 I48385	RNA helicase TN22
38	31	77.5	614	2 JC1087	RNA helicase, ATP-
39	31	77.5	668	2 T10575	hypothetical prote
40	31	77.5	825	2 S55060	feritin alpha-II
41	31	77.5	893	2 T03864	hypothetical prote
42	31	77.5	905	2 S55059	feritin alpha-I
43	30	75.0	182	2 AE2146	hypothetical prote
44	30	75.0	194	2 T22209	hypothetical prote
45	30	75.0	229	2 A89473	protein F52D2.2 [i

ALIGNMENTS

RESULT 1

JK0201

alpha-amylase (EC 3.2.1.1) - Aspergillus oryzae

N:Alternate names: glycogenase; Taka-amylase A

C:Species: Aspergillus oryzae

C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004

C:Accession: JK0201

R: Toda, H.; Kondo, K.; Narita, K.

Proc. Jpn. Acad. 58B, 208-212, 1982

A: Title: The complete amino acid sequence of Taka-amylase A.

A: Reference number: JK0201

A: Accession: JK0201

A: Molecule type: protein

A: Residues: 1-478 <TOD>

A: Cross-references: UNIPROT: P10529

C: Comment: One atom of calcium per molecule is essential for the activity.

C: Comment: This enzyme is a glycoprotein.

C: Comment: See also PIR:JT0466 and PIR:JS0240.

C: Function:

A: Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A: Pathway: glycogen/starch degradation

C: Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C: Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F: 173-300/Domain: alpha-amylase core homology <AMY>

F: 197/Binding site: carbohydrate (Asn) (covalent) #status experimental

F: 210,230,297/Active site: His, Glu, Asp #status experimental

Query Match 100.0%; Score 40; DB 2; Length 478;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7

Db 141 SSQDYFH 147

RESULT 2

A48305

alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori

C: Species: Aspergillus awamori

C: Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C: Accession: A48305

R: Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;

Curr. Genet. 17, 203-212, 1990

A: Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe

A: Reference number: A48305; MUID: 90254827; PMID: 2340591

A: Accession: A48305

A: Status: preliminary; not compared with conceptual translation

A: Molecule type: DNA

A: Residues: 1-498 <KOR>

A: Cross-references: UNIPROT: Q02905

C: Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology <AMY>
Query Match 100.0%; Score 40; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.5; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;
QY 1 SSQDYFH 7
Db 162 SSQDYFH 168
RESULT 3
ALAS1
Alpha-amylase (EC 3.2.1.1) 1 precursor [validated] - Aspergillus oryzae
N;Alternate names: alpha-amylase isozyme II; glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
C;Accession: S04548; A33214; J50240; A91930; A93767; A10627
R;Wirsfel, S.; Lachmund, A.; Wildhardt, G.; Rutkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon c
A;Reference number: S04548; MUID:89237897; PMID:2785629
A;Accession: S04548
A;Molecule type: DNA
A;Residues: 1-499 <WIR>
A;Cross-references: UNIPROT:P10529; EMBL:X12725; NID:g2430; PIDN:CAA31218.1; PID:g295921
A;Genetics: AMY1
A;Accession: A33214
A;Molecule type: mRNA
A;Residues: 1-499 <W12>
A;Cross-references: GB:X12725; NID:g2430; PIDN:CAA31218.1; PID:g295921
R;Genes, M.J.; Dove, M.J.; Seligy, V.L.
Gene 79, 107-117, 1989
A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing
A;Reference number: J50240; MUID:89378767; PMID:2789162
A;Accession: J50240
A;Molecule type: DNA
A;Residues: 1-499 <GEN>
A;Cross-references: A91930; MUID:74001521; PMID:4733850
A;Accession: A91930
A;Molecule type: protein
A;Residues: 206-225 <ISE>
R;Narita, K.
Proc. Jpn. Acad. 51, 285-290, 1975
A;Reference number: A93767
A;Accession: A93767
A;Molecule type: protein
A;Residues: 434-443, 446-447, 'Q', 449-458, 'GTVV', 459-464, 467-468, 'B', 470, 'B', 472-499 <NAR>
R;Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
A;Title: Structure and possible catalytic residues of Taka-amylase A.
A;Reference number: A37454; MUID:84212370; PMID:6609921
A;Contents: annotation; X-ray crystallography, 3.0 angstroms
R;Swift, H.J.; Brady, L.; Derewenda, Z.S.; Dodson, E.J.; Turkenbourg, J.P.; Wilkinson, A.
submitted to the Brookhaven Protein Data Bank, August 1992
A;Reference number: A51548; PDB:16TAA
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 22-497
C;Comment: One atom of calcium per molecule is essential for activity.
C;Genetics: <AMY1>
A;Gene: amy1
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Genetics: <AMY2>
A;Gene: amy2; AmyII
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; polys
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase 1 #status experimental <MAT>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
F;142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;227,251,318/Active site: Asp, Glu, Asp #status predicted
Query Match 100.0%; Score 40; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.5; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;
QY 1 SSQDYFH 7
Db 162 SSQDYFH 168
RESULT 4
ALAS3
Alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae
N;Alternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
C;Accession: S04549; A33215; A44713
R;Wirsfel, S.; Lachmund, A.; Wildhardt, G.; Rutkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon c
A;Reference number: S04548; MUID:89237897; PMID:2785629
A;Accession: S04549
A;Molecule type: DNA
A;Residues: 1-499 <WIR>
A;Cross-references: UNIPROT:Q96TH4; EMBL:X12727; NID:g2454; PIDN:CAA31220.1; PID:g295922
A;Accession: A33215
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-499 <W12>
A;Cross-references: GB:X12727; NID:g2454; PIDN:CAA31220.1; PID:g295922
R;Genes, M.J.; Dove, M.J.; Seligy, V.L.
Gene 79, 107-117, 1989
A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing
A;Reference number: J50240; MUID:89378767; PMID:2789162
A;Accession: A44713
A;Molecule type: DNA
A;Residues: 1-499 <GEN>
A;Note: the authors refer to this as isozyme I
R;Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
A;Title: Structure and possible catalytic residues of Taka-amylase A.
A;Reference number: A37454; MUID:84212370; PMID:6609921
A;Contents: annotation; X-ray crystallography, 3.0 angstroms
C;Comment: One atom of calcium per molecule is essential for activity.
C;Genetics: <AMY1>
A;Gene: amy3; AmyI
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; metal
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase 3 #status experimental <AMY>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
F;142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;227,251,318/Active site: His, Glu, Asp #status experimental
Query Match 100.0%; Score 40; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.5;

```

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 5
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus sp.
N:Alternate names: Aspergillus sp.
C:Species: Aspergillus sp.
C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
C:Accession: J00663
R:Shibuya, I.; Tamura, G.; Ishikawa, T.; Hara, S.
Biosci. Biotechnol. Biochem. 56, 174-179, 1992
A:Title: Cloning of the alpha-amylase cDNA of Aspergillus shiroyamii and its expression
A:Reference number: J00663; MUID:92323146; PMID:1368777
A:Accession: J00663
A:Molecule type: mRNA
A:Residues: 1-499 <SHI>
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-499/Product: alpha-amylase #status predicted <ALP>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:218/Binding site: carbohydrate (Asn) #status predicted
Query Match 100.0%; Score 40; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 6
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N:Alternate names: glycogenase; Taka-amylase A
C:Species: Aspergillus oryzae
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: J00466
R:Tada, S.; Iimura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.
Agric. Biol. Chem. 53, 593-599, 1989
A:Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergillus
A:Reference number: J00466
A:Accession: J00466
A:Molecule type: DNA
A:Residues: 1-499 <TAD>
A:Cross-references: UNIPROT:P10529
C:Comment: See also PIR:JK0201 and PIR:JS0240.
C:Comment: One atom of calcium per molecule is essential for activity.
C:Genetics:
A:Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-499/Product: alpha-amylase #status predicted <MAT>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:218/Binding site: carbohydrate (Asn) #status predicted
F:231.251.318/Active site: His, Glu, Asp #status predicted
Query Match 100.0%; Score 40; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 7
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N:Alternate names: Taka-amylase A
C:Species: Aspergillus oryzae
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: JN0588
R:Tsuikagoshi, N.; Furukawa, M.; Nagaba, H.; Kiritani, N.; Tsuboi, A.; Uda, S.
Gene 84, 319-327, 1989
A:Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for m
A:Reference number: JN0588; MUID:90128276; PMID:2612911
A:Accession: JN0588
A:Molecule type: mRNA
A:Residues: 1-499 <TSU>
A:Cross-references: UNIPROT:Q96TH4
C:Comment: The alpha amylases are encoded by multigene family.
C:Genetics:
A:Gene: Taa-G1
A:Introns: 56/1; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-499/Product: alpha-amylase #status predicted <MAT>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:218/Binding site: carbohydrate (Asn) #status predicted
Query Match 100.0%; Score 40; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 8
alpha-amylase (EC 3.2.1.1) B precursor - Aspergillus awamori
C:Species: Aspergillus awamori
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: B48305
R:Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A:Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe
A:Reference number: B48305; MUID:90254827; PMID:2340591
A:Accession: B48305
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-499 <KOR>
A:Cross-references: UNIPROT:Q02906
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:194-321/Domain: alpha-amylase core homology <AMY>
Query Match 100.0%; Score 40; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

```

RESULT 9
 JC4510
 pullulanase (EC 3.2.1.41) precursor - yeast (*Lipomyces kononenkoae*)
 N:Alternate names: LKA1 protein; raw starch-degrading amylase
 N:Contains: alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)
 C:Species: *Lipomyces kononenkoae*
 C:Date: 07-Feb-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
 C:Accession: JC4510; PC4116
 R:Steyn, A.J.C.; Marmur, J.; Pretorius, I.S.
 Gene 166, 65-71, 1995
 A:Title: Cloning, sequence analysis and expression in yeasts of a cDNA containing a LipD
 A:Reference number: JC4510; MUID:96105202; PMID:8529895
 A:Accession: JC4510
 A:Molecule type: mRNA
 A:Residues: 1-624 <STE>
 A:Cross-references: UNIPROT:Q01117; GB:U030376; NID:g1173536; PIDN:AAC49622.1; PID:g11735
 A:Experimental source: strain IGC4052B
 A:Accession: PC4116
 A:Molecule type: protein
 A:Residues: 29-44 <ST2>
 A:Experimental source: IGC4052B
 C:Genetics:
 A:Gene: LKA1
 C:Function:
 A:Description: hydrolyzes raw starch, degrading both alpha-1,4 and alpha-1,6 linkages
 A:Pathway: glycogen/starch degradation
 C:Superfamily: lipomyces alpha-amylase; alpha-amylase core homology; glucoamylase starch
 C:Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-624/Product: alpha-amylase #status predicted <MAT>
 F:48-141/Domain: glucoamylase starch-binding domain homology <SBD>
 F:320-447/Domain: alpha-amylase core homology <AMY>
 F:177-185,297-311,387-430,587-622/Disulfide bonds: #status predicted
 F:304,344/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:357,377,444/Active site: His, Glu, Asp #status predicted

Query Match 100.0%; Score 40; DB 1; Length 624;
 Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

QY 1 SSQDYFH 7
 |||||
 DB 288 SSQDYFH 294

RESULT 10
 H71415
 hypothetical protein - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 A:Variety: Columbia
 C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
 C:Accession: H71415
 R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
 P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terry, N.; Giel
 vanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
 Nature 391, 485-488, 1998
 A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
 erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, V.; Palme, K.; Benes, V.; Rechman, S.; Ans
 C.; Chalwatzis, N.
 A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of *Arabidopsis thal*
 A:Reference number: A71400; MUID:98121113; PMID:9461215
 A:Accession: H71415
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-130 <BEV>
 A:Cross-references: UNIPROT:Q23373; GB:Z97338; NID:g2244870; PID:e326912; PID:g2244877
 C:Genetics:
 A:Map position: 4COP9-4G3845

Query Match 85.0%; Score 34; DB 2; Length 130;
 Best Local Similarity 85.7%; Pred. No. 6.1; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0;

QY 1 SSQDYFH 7
 |||||
 DB 38 SSADYFH 44

RESULT 11
 T42616
 envelope protein - equine herpesvirus 4 (strain NS80567)
 C:Species: equine herpesvirus 4
 A:Variety: strain NS80567
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T42616
 R:Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
 J. Gen. Virol. 79, 1197-1203, 1998
 A:Title: The DNA sequence of equine herpesvirus-4.
 A:Reference number: Z22173; MUID:98264497; PMID:9603335
 A:Accession: T42616
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-420 <TEL>
 A:Cross-references: UNIPROT:O39309; EMBL:AF030027; NID:g2605950; PIDN:AAC59593.1; PID:g2
 A:Experimental source: strain NS80567
 C:Genetics:
 A:Note: 73
 C:Superfamily: pseudorabies virus glycoprotein gp63

Query Match 82.5%; Score 33; DB 2; Length 420;
 Best Local Similarity 83.3%; Pred. No. 36; Mismatches 1; Indels 0; Gaps 0;
 Matches 5; Conservative 1;

QY 2 SODYFH 7
 :|||||
 DB 114 NODYFH 119

RESULT 12
 T18787
 hypothetical protein BE10.3 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T18787
 R:McMurray, A.
 submitted to the EMBL Data Library, March 1997
 A:Reference number: Z19022
 A:Accession: T18787
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-601 <WIL>
 A:Cross-references: UNIPROT:O17552; EMBL:Z93372; PIDN:CAB07545.1; GSPDB:GN00021; CBSP:BE1
 A:Experimental source: clone BE10
 C:Genetics:
 A:Gene: CESP:BE10.3
 A:Map position: 3
 A:Introns: 21/3; 54/3; 117/2; 157/1; 212/2; 533/3

Query Match 82.5%; Score 33; DB 2; Length 601;
 Best Local Similarity 71.4%; Pred. No. 53; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 2;

QY 1 SSQDYFH 7
 :|||||
 DB 453 NSQDYFH 459

RESULT 13
 T41943
 major DNA binding protein - human herpesvirus 7 (strain JI)
 C:Species: human herpesvirus 7
 A:Variety: strain JI
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T41943
 R:Nicholas, J.

submitted to the EMBL Data Library, December 1995

A;Description: Determination and analysis of the complete nucleotide sequence of human h
A;Reference number: Z22022
A;Accession: T41943
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1131 <NIC>
A;Cross-references: UNIPROT:P52339; EMBL:U43400; PIDN:AAC54703.1
A;Experimental source: strain JI
C;Genetics:
A;Note: U41
C;Superfamily: herpesvirus DNA-binding protein

Query Match 82.5%; Score 33; DB 2; Length 1131;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7

:|||||

Db 943 ASRDYFH 949

RESULT 14

T00252

MEGF1 protein - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

C;Accession: T00252

R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.

Genomics 51, 27-34, 1998

A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs

A;Reference number: Z14126; MUID:98360089; PMID:9693030

A;Accession: T00252

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-4351 <NAK>

A;Cross-references: UNIPROT:O88277; EMBL:AB011527; NID:G3449285; PIDN:BAA32458.1; PID:G3

A;Experimental source: brain

C;Genetics:

A;Gene: MEGF1

C;Superfamily: rat MEGF1 protein; cadherin repeat homology; EGF homology; laminin G repe

F;3798-3949/Domain: laminin G repeat homology <LGR>

F;3953-3985/Domain: EGF homology <EGF>

F;3992-4023/Domain: EGF homology <EGF1>

Query Match 82.5%; Score 33; DB 2; Length 4351;

Best Local Similarity 71.4%; Pred. No. 4.6e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSQDYFH 7

:|||||

Db 605 NEQDYFH 611

RESULT 15

JC7121

androgenic gland hormone precursor - common pill bug

C;Species: Armadillidium vulgare (common pill bug)

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C;Accession: JC7121

R;Okuno, A.; Hasegawa, Y.; Ohira, T.; Katakura, Y.; Nagasawa, H.

Biochem. Biophys. Res. Commun. 264, 419-423, 1999

A;Title: Characterization and cDNA cloning of androgenic gland hormone of the terrestria

A;Reference number: JC7121; MUID:20001935; PMID:10529379

A;Accession: JC7121

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-144 <OKU>

A;Cross-references: UNIPROT:Q9U8R2; DBJ:AB029615; GB:AB029615; NID:G6446571; PID:G64465

A;Experimental source: androgenic gland

Query Match

Best Local Similarity 80.0%; Score 32; DB 2; Length 144;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDYFH 7

|||||

Db 82 QDYFH 86

Search completed: November 7, 2005, 18:58:46

Job time : 1.81081 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:58:04 ; Search time 6.95174 Seconds.
(without alignments)
782.441 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110
Perfect score: 13
Sequence: 1 AYHGYWQDDIYSL 13

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867879 seqs, 418409474 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	476	17	US-10-877-849-43
2	13	100.0	478	14	US-10-184-771-10
3	13	100.0	478	14	US-10-186-042-7
4	13	100.0	478	15	US-10-644-187-7
5	13	100.0	478	17	US-10-926-720-10
6	13	100.0	478	17	US-10-980-759-7
7	13	100.0	478	20	US-11-064-196-10
8	13	100.0	498	16	US-10-815-495-22
9	13	100.0	498	16	US-10-820-200-2
10	13	100.0	498	17	US-10-877-849-30
11	13	100.0	499	16	US-10-815-495-18

12	13	100.0	499	16	US-10-797-393A-5	Sequence 5, Appli
13	13	100.0	608	17	US-10-877-849-40	Sequence 40, Appl
14	13	100.0	640	17	US-10-877-849-36	Sequence 36, Appl
15	13	100.0	1095	14	US-10-228-063-45	Sequence 45, Appl
16	12	92.3	495	14	US-10-213-990-42	Sequence 42, Appl
17	9	69.2	494	17	US-10-486-868-13	Sequence 13, Appl
18	8	61.5	484	15	US-10-416-393-1	Sequence 1, Appli
19	8	61.5	484	16	US-10-797-393A-1	Sequence 1, Appli
20	8	61.5	505	17	US-10-877-849-42	Sequence 42, Appl
21	8	61.5	511	17	US-10-877-849-8	Sequence 8, Appli
22	8	61.5	609	17	US-10-877-849-38	Sequence 38, Appl
23	8	61.5	629	17	US-10-877-849-34	Sequence 34, Appl
24	8	61.5	640	17	US-10-877-007-22	Sequence 22, Appl
25	8	61.5	640	17	US-10-877-849-32	Sequence 32, Appl
26	8	61.5	640	17	US-10-877-849-41	Sequence 41, Appl
27	7	53.8	630	14	US-10-213-990-45	Sequence 45, Appl
28	6	46.2	175	15	US-10-424-599-258851	Sequence 258851,
29	6	46.2	190	16	US-10-425-115-279730	Sequence 279730,
30	6	46.2	252	16	US-10-425-115-239140	Sequence 239140,
31	6	46.2	429	15	US-10-369-493-22639	Sequence 22639, A
32	6	46.2	483	15	US-10-369-493-597	Sequence 597, App
33	6	46.2	493	15	US-10-369-493-22723	Sequence 22723, A
34	6	46.2	500	15	US-10-369-493-12469	Sequence 12469, A
35	6	46.2	513	15	US-10-369-493-2223	Sequence 2223, Ap
36	6	46.2	547	14	US-10-213-990-48	Sequence 48, Appl
37	6	46.2	549	17	US-10-486-868-14	Sequence 14, Appl
38	6	46.2	555	17	US-10-486-868-15	Sequence 15, Appl
39	6	46.2	564	15	US-10-369-493-22679	Sequence 22679, A
40	6	46.2	567	17	US-10-486-868-18	Sequence 18, Appl
41	6	46.2	583	17	US-10-732-923-7439	Sequence 7439, Ap
42	6	46.2	647	17	US-10-732-923-7480	Sequence 7480, Ap
43	6	46.2	686	17	US-10-872-198-44	Sequence 44, Appl
44	6	46.2	686	17	US-10-872-197A-44	Sequence 44, Appl
45	6	46.2	686	18	US-10-787-219A-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-10-877-849-43
; Sequence 43, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877, 849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 43
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)..(476)
US-10-877-849-43

Query Match 100.0%; Score 13; DB 17; Length 476;
Best Local Similarity 100.0%; Pred.No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AYHGYWQDDIYSL 13
DB 78 AYHGYWQDDIYSL 90

RESULT 2
US-10-184-771-10
; Sequence 10, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1f216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-10-184-771-10

Query Match 100.0%; Score 13; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDDIYSL 13
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Db 78 AYHGYWQDDIYSL 90

RESULT 3
US-10-186-042-7
; Sequence 7, Application US/10186042
; Publication No. US20030171236A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match 100.0%; Score 13; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDDIYSL 13
| | | | | | | | | | | | | | |
Db 78 AYHGYWQDDIYSL 90

RESULT 4
US-10-644-187-7
; Sequence 7, Application US/10644187
; Publication No. US20040048351A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/644,187
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-644-187-7

Query Match 100.0%; Score 13; DB 15; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDDIYSL 13
| | | | | | | | | | | | | | |
Db 78 AYHGYWQDDIYSL 90

RESULT 5
US-10-926-720-10
; Sequence 10, Application US/10926720
; Publication No. US20050019886A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/926,720
; FILING DATE: 26-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475

REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10

Query Match 100.0%; Score 13; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
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Db 78 AYHGYWQDDIYSL 90

RESULT 6

US-10-980-759-7
Sequence 7, Application US/10980759
Publication No. US20050118695A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/980,759
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 478
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-980-759-7

Query Match 100.0%; Score 13; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
|||||
Db 78 AYHGYWQDDIYSL 90

RESULT 7

US-11-064-196-10
Sequence 10, Application US/11064196
Publication No. US20050170487A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants

FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/11/064,196
CURRENT FILING DATE: 2005-02-22
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 478
TYPE: PRT
ORGANISM: A. oryzae
US-11-064-196-10

Query Match 100.0%; Score 13; DB 20; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
|||||
Db 78 AYHGYWQDDIYSL 90

RESULT 8

US-10-815-495-22
Sequence 22, Application US/10815495
Publication No. US20040191864A1
GENERAL INFORMATION:
APPLICANT: Novozymes Biotech, Inc.
APPLICANT: Connolly, Mariah
APPLICANT: Brody, Howard
TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
TITLE OF INVENTION: Mutants Of Aspergillus Niger
FILE REFERENCE: 10345.200-US
CURRENT APPLICATION NUMBER: US/10/815,495
CURRENT FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 498
TYPE: PRT
ORGANISM: Aspergillus niger
US-10-815-495-22

Query Match 100.0%; Score 13; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
|||||
Db 99 AYHGYWQDDIYSL 111

RESULT 9

US-10-820-200-2
Sequence 2, Application US/10820200
Publication No. US20040229764A1
GENERAL INFORMATION:
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Pedersen, Sven
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
FILE REFERENCE: 5835.200-US
CURRENT APPLICATION NUMBER: US/10/820,200
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US/09/710,339
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/165,786
PRIOR FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2

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; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus Oryzae
US-10-820-200-2

Query Match      100.0%; Score 13; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
|||||
DB 98 AYHGYWQDDIYSL 110
|||||

RESULT 10
US-10-877-849-30
; Sequence 30, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-877-849-30

Query Match      100.0%; Score 13; DB 17; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
|||||
DB 98 AYHGYWQDDIYSL 110
|||||

RESULT 11
US-10-815-495-18
; Sequence 18, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connelly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-18

Query Match      100.0%; Score 13; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
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DB 99 AYHGYWQDDIYSL 111

RESULT 12
US-10-797-393A-5
; Sequence 5, Application US/10797393A
; Publication No. US20040219649A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Hans Sejr
; APPLICANT: Pedersen, Sven
; APPLICANT: Feestersen, Rikke Monica
; TITLE OF INVENTION: ALCOHOL PRODUCT PROCESSES
; FILE REFERENCE: 10391.200-US
; CURRENT APPLICATION NUMBER: US/10/797,393A
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-797-393A-5

Query Match      100.0%; Score 13; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
|||||
DB 99 AYHGYWQDDIYSL 111
|||||

RESULT 13
US-10-877-849-40
; Sequence 40, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-40

Query Match      100.0%; Score 13; DB 17; Length 608;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
|||||
DB 98 AYHGYWQDDIYSL 110
|||||

RESULT 14
US-10-877-849-36
; Sequence 36, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
```

; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-36

Query Match 100.0%; Score 13; DB 17; Length 640;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
|||
Db 98 AYHGYWQDIYSL 110

RESULT 15
US-10-228-063-45
; Sequence 45, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lananan, Mike
; TITLE OF INVENTION: Self-processing plants and plant parts
; FILE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Aspergillus shirousami
US-10-228-063-45

Query Match 100.0%; Score 13; DB 14; Length 1095;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
|||
Db 78 AYHGYWQDIYSL 90

Search completed: November 7, 2005, 19:22:50
Job time : 7.95174 secs

Large black (1904)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2005, 18:45:18 ; Search time 1.95753 Seconds
(without alignments)
495.746 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110
Perfect score: 13
Sequence: 1 AVHGWQDIYSL 13

Scoring table: OLIGO
Gapex 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*
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6: /cgn2.6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	478	1 US-08-720-899-7	Sequence 7, Appli
2	13	100.0	478	1 US-08-459-610-7	Sequence 7, Appli
3	13	100.0	478	2 US-08-343-804-7	Sequence 7, Appli
4	13	100.0	478	2 US-08-600-908A-10	Sequence 10, Appl
5	13	100.0	478	3 US-08-683-838A-10	Sequence 10, Appl
6	13	100.0	478	3 US-09-182-859-7	Sequence 7, Appli
7	13	100.0	478	4 US-09-672-459-7	Sequence 7, Appli
8	13	100.0	478	4 US-09-636-252A-10	Sequence 10, Appl
9	13	100.0	478	4 US-10-186-042-7	Sequence 7, Appli
10	6	46.2	14	1 US-08-204-656B-11	Sequence 11, Appl
11	6	46.2	14	1 US-08-204-656B-12	Sequence 12, Appl
12	6	46.2	14	1 US-08-470-702-11	Sequence 11, Appl
13	6	46.2	14	1 US-08-470-702-12	Sequence 12, Appl
14	6	46.2	14	1 US-08-467-831-11	Sequence 11, Appl
15	6	46.2	14	1 US-08-467-831-12	Sequence 12, Appl
16	6	46.2	31	1 US-08-190-802A-234	Sequence 234, App
17	6	46.2	31	3 US-08-477-346-234	Sequence 234, App
18	6	46.2	31	3 US-08-473-089-234	Sequence 234, App
19	6	46.2	31	4 US-08-487-072A-234	Sequence 234, App
20	6	46.2	394	4 US-09-248-796A-18703	Sequence 18703, A
21	6	46.2	514	4 US-09-108-857-2	Sequence 2, Appli
22	6	46.2	685	3 US-08-947-965-72	Sequence 72, Appl
23	6	46.2	685	3 US-08-947-965-74	Sequence 74, Appl
24	6	46.2	686	3 US-08-947-965-70	Sequence 70, Appl
25	6	46.2	686	3 US-08-947-965-73	Sequence 73, Appl
26	6	46.2	713	1 US-08-190-802A-63	Sequence 63, Appl
27	6	46.2	713	3 US-08-477-346-63	Sequence 63, Appl

28	6	46.2	713	3	US-08-473-089-63	Sequence 63, Appl
29	6	46.2	713	4	US-08-487-072A-63	Sequence 63, Appl
30	6	46.2	713	4	US-09-108-857-3	Sequence 3, Appli
31	6	46.2	833	3	US-09-514-302-3	Sequence 3, Appli
32	6	46.2	833	4	US-10-014-436-3	Sequence 3, Appli
33	6	46.2	1938	3	US-09-514-302-2	Sequence 2, Appli
34	6	46.2	1938	4	US-10-014-436-2	Sequence 2, Appli
35	5	38.5	8	4	US-09-108-857-7	Sequence 7, Appli
36	5	38.5	13	2	US-08-870-864-2	Sequence 2, Appli
37	5	38.5	30	4	US-09-471-276-1105	Sequence 1105, Ap
38	5	38.5	61	3	US-08-858-207A-538	Sequence 538, App
39	5	38.5	87	4	US-09-583-110-3205	Sequence 3205, Ap
40	5	38.5	90	4	US-09-107-433-4734	Sequence 4734, Ap
41	5	38.5	129	4	US-10-101-464A-609	Sequence 609, App
42	5	38.5	131	4	US-09-270-767-32792	Sequence 32792, A
43	5	38.5	131	4	US-09-270-767-48009	Sequence 48009, A
44	5	38.5	133	4	US-10-101-464A-485	Sequence 485, App
45	5	38.5	136	4	US-09-270-767-32469	Sequence 32469, A

ALIGNMENTS

RESULT 1
US-08-720-899-7
; Sequence 7, Application US/08720899
; Patent No. 5753460
; GENERAL INFORMATION:
; APPLICANT: Biggaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 57534600 No. 5753460disk of No. 5753460th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,899
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-720-899-7

Query Match 100.0%; Score 13; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 AYHGYWQDDIYSL 13
Db 78 AYHGYWQDDIYSL 90

RESULT 2
US-08-459-610-7
; Sequence 7, Application US/08459610
; Patent No. 5801043
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5801043o No. 5801043disk of No. 5801043th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,610
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-459-610-7

Query Match 100.0%; Score 13; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDDIYSL 13
Db 78 AYHGYWQDDIYSL 90

RESULT 3
US-08-343-804-7
; Sequence 7, Application US/08343804
; Patent No. 580837
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 580837o No. 580837disk of No. 580837th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-459-610-7

Query Match 100.0%; Score 13; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDDIYSL 13
Db 78 AYHGYWQDDIYSL 90

RESULT 4
US-08-600-908A-10
; Sequence 10, Application US/08600908A
; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: '-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5989169o No. 5989169disk of No. 5989169th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-343-804-7

Query Match 100.0%; Score 13; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDDIYSL 13
Db 78 AYHGYWQDDIYSL 90

RESULT 5
US-08-600-908A-10
; Sequence 10, Application US/08600908A
; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: '-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5989169o No. 5989169disk of No. 5989169th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-343-804-7
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-600-908A-10

Query Match          100.0%; Score 13; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYWQDDIYSL 13
Db      78 AYHGYWQDDIYSL 90

RESULT 5
US-08-683-838A-10
; Sequence 10, Application US/08683838A
; Patent No. 6022724
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Prantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: '-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6022724o No. 6022724disk of No. 6022724th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,838A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-683-838A-10

Query Match          100.0%; Score 13; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYWQDDIYSL 13
Db      78 AYHGYWQDDIYSL 90

RESULT 6
US-09-182-859-7
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; Sequence 7, Application US/09182859
; Patent No. 6143708
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Prantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/182,859
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: 0515/96
; EARLIER FILING DATE: 1996-04-30
; EARLIER APPLICATION NUMBER: 0712/96
; EARLIER FILING DATE: 1996-06-28
; EARLIER APPLICATION NUMBER: 0775/96
; EARLIER FILING DATE: 1996-07-11
; EARLIER APPLICATION NUMBER: 1263/96
; EARLIER FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-182-859-7

Query Match          100.0%; Score 13; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYWQDDIYSL 13
Db      78 AYHGYWQDDIYSL 90

RESULT 7
US-09-672-459-7
; Sequence 7, Application US/09672459
; Patent No. 6436888
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Prantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/672,459
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-672-459-7

Query Match          100.0%; Score 13; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYWQDDIYSL 13
Db      78 AYHGYWQDDIYSL 90
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RESULT 8
US-09-636-252A-10
; Sequence 10, Application US/09636252A
; Patent No. 6440716
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/09/636,252A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-09-636-252A-10

Query Match      100.0%; Score 13; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYWQDDIYSL 13
DB      78 AYHGYWQDDIYSL 90

RESULT 9
US-10-186-042-7
; Sequence 7, Application US/10186042
; Patent No. 6642044
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1995-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match      100.0%; Score 13; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYWQDDIYSL 13
DB      78 AYHGYWQDDIYSL 90
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RESULT 10
US-08-204-656B-11
; Sequence 11, Application US/08204656B
; Patent No. 5538882
; GENERAL INFORMATION:
; APPLICANT: Matsui, Ikuro
; APPLICANT: Ishikawa, Kazuhiko
; APPLICANT: Miyairi, Sachio
; APPLICANT: Honda, Koichi
; TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase.
; TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
; TITLE OF INVENTION: Oligosaccharide Using The Enzyme
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,656B
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiner, Marc S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-204-656B-11

Query Match      46.2%; Score 6; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYW 6
DB      7 AYHGYW 12

RESULT 11
US-08-204-656B-12
; Sequence 12, Application US/08204656B
; Patent No. 5538882
; GENERAL INFORMATION:
; APPLICANT: Matsui, Ikuro
; APPLICANT: Ishikawa, Kazuhiko
; APPLICANT: Miyairi, Sachio
; APPLICANT: Honda, Koichi
; TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase.
; TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
; TITLE OF INVENTION: Oligosaccharide Using The Enzyme
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
```

```
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,656B
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-204-656B-12

Query Match 46.2%; Score 6; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYW 6
Db 7 AYHGYW 12

RESULT 12
US-08-470-702-11
; Sequence 11, Application US/08470702
; Patent No. 5631149
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKUO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
; TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
; TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
; TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,702
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/204,656
; FILING DATE: 02-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-204-656B-12

Query Match 46.2%; Score 6; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYW 6
Db 7 AYHGYW 12

RESULT 13
US-08-470-702-12
; Sequence 12, Application US/08470702
; Patent No. 5631149
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKUO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
; TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
; TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
; TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,702
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/204,656
; FILING DATE: 02-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-470-702-11
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; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
;

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Query Match 46.2%; Score 6; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 0; Indels

Qy 1 AYHGYW 6
7 AYHGYW 12

```

RESULT 14
US-08-467-831-11
; Sequence 11, Application US/08467831
; Patent No. 5635378
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKUO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
; TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
; TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
; TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:

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Query Match	46.2%	Score 6;	DB 1;	Length 14;
Best Local Similarity	100.0%	Pred. No. 1.3;		

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AVHGYW 6
    |||||
Db 7 AVHGYW 12

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RESULT 15
US-08-467-831-12
; Sequence 12, Application US/08467831
; Patent No. 5635378
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKUO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
; TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
; TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
; TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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Query Match          46.2%; Score 6; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches             6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AYHGYW 6
7 AYHGYW 12

Search completed: November 7, 2005, 19:00:09
Job time : 2.95753 secs

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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:25:16 ; Search time 291.301 Seconds
(without alignments)
661.194 Million cell updates/sec

Title: US-10-820-200-2
Perfect score: 2684
Sequence: 1 NVAWWSFLYGLQVAPALA.....LPRVLYPTKLAGSKICSSS 498

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A: Geneseq 16Dec04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2684	100.0	498	AAB84206	AAB84206 Amino aci
2	2674	99.6	499	ADT89628	ADT89628 Aspergill
3	2662	99.2	498	ADT89632	ADT89632 Aspergill
4	2572	95.8	478	AAR72450	AAR72450 Aspergill
5	2572	95.8	478	AAR78270	AAR78270 Aspergill
6	2572	95.8	478	AAW14500	AAW14500 Aspergill
7	2569	95.7	1095	ABP96630	ABP96630 Alpha-amyl
8	2552	95.1	478	AAR46065	AAR46065 Mutant al
9	2503.5	93.3	478	AAR79025	AAR79025 Mature ta
10	2151	80.1	423	ABB09072	ABB09072 Aspergill
11	2100	78.2	495	ABB80177	ABB80177 A. fumiga
12	2012	75.0	494	ABP97894	ABP97894 Amino aci
13	1835	68.4	630	ABB80178	ABB80178 A. fumiga
14	1778	66.2	484	AAE24207	AAE24207 Aspergill
15	1778	66.2	484	ADS75939	ADS75939 Aspergill
16	1666.5	62.1	493	AAR88212	AAR88212 Alpha-amyl
17	1449	54.0	512	AAR07574	AAR07574 Alpha-amyl
18	1400.5	52.2	511	AAP81180	AAP81180 Sequence
19	1398.5	52.1	511	AAR81161	AAR81161 Recombina
20	1397	52.0	468	AAR24136	AAR24136 Alpha-amyl
21	1396.5	52.0	494	AAP70571	AAP70571 Alpha-amyl
22	1392	51.9	468	AAR63184	AAR63184 Variant a
23	1391	51.8	468	AAR63185	AAR63185 Variant a
24	1387	51.7	468	AAR63187	AAR63187 Variant a
25	1338	49.9	452	AAR63186	AAR63186 Variant a

26	1214.5	45.2	547	6	ABB80179	ABB80179 A. fumiga
27	1183	44.1	555	6	ABP97896	ABP97896 Amino aci
28	1163	43.3	567	6	ABP97899	ABP97899 Amino aci
29	1160	43.2	500	8	ADS23436	ADS23436 Bacterial
30	1085	40.4	549	6	ABP97895	ABP97895 Amino aci
31	1015.5	37.8	513	8	ADN19570	ADN19570 Bacterial
32	898.5	33.5	564	8	ADS44249	ADS44249 Bacterial
33	873	32.5	493	8	ADS44293	ADS44293 Bacterial
34	541	20.2	502	6	ABU03092	ABU03092 Alpha amy
35	483.5	18.0	547	8	ADS30907	ADS30907 Bacterial
36	480.5	17.9	547	8	ADC30029	ADC30029 Bacterial
37	456.5	17.0	713	7	ADC23483	ADC23483 Bacillus
38	453	16.9	719	4	AAE74220	AAE74220 Bacillus
39	452.5	16.9	712	2	AAR10051	AAR10051 Cyclomalt
40	452	16.8	719	4	AAE74219	AAE74219 Bacillus
41	450	16.8	719	2	AAV31731	AAV31731 Bacillus
42	450	16.8	719	2	AAV30621	AAV30621 Amino aci
43	450	16.8	719	3	AAV94271	AAV94271 Bacillus
44	450	16.8	719	4	AAE59956	AAE59956 Bacillus
45	450	16.8	719	4	AAE74216	AAE74216 Bacillus

ALIGNMENTS

RESULT 1

AAAB84206
ID AAB84206 standard; protein; 498 AA.
XX AC AAB84206;
XX DT 06-AUG-2001 (first entry)
XX DE Amino acid sequence of a fungamyl-like alpha-amylase.
XX KW Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose;
XX KW alcohol; starch; dough improver; brewing; starch liquification.
XX OS Aspergillus oryzae.
XX PN WO200134784-A1.
XX PD 17-MAY-2001.
XX PF 10-NOV-2000; 2000WO-DK000626.
XX PR 10-NOV-1999; 99DK-00001617.
XX PA (NOVO) NOVOZYMES AS.
XX PI Bisgard-Frantzen H, Svendsen A, Pedersen S;
XX DR WPI; 2001-367478/38.
XX DR N-PSDB; AAF90208.
XX PT New variant of Fungamyl-like alpha-amylase, useful for production of
PT maltose syrups, includes mutations that improve stability against heat
PT and acidic pH.
XX PS Claim 1; Page 42-45; 49pp; English.
XX CC The present sequence represents a fungamyl-like alpha-amylase. The
CC specification describes variants of this fungamyl-like alpha-amylase,
CC which have an alteration in one the amino acid regions 98-110, 150-160,
CC 161-167, 280-288, 448-455, and 468-475. Each alteration is a deletion or
CC substitution of an amino acid or an insertion of an amino acid downstream
CC of a particular position. The variants retain alpha-amylase activity, and
CC have better heat stability and/or stability at acidic pH, relative to
CC wild-type enzyme. The variants can therefore be used at higher
CC temperatures (more efficient conversion or faster reaction, and have
CC reduced need for cooling and reduced risk of contamination). The variants
CC may also be used in conjunction with other enzymes, particularly
CC glucoamylase during dextrinisation. The variants are used to produce

CC syrups, particularly of high maltose content, or alcohol, from starch; as
 CC dough improver for baked goods; in brewing, to increase fermentability of
 CC the wort; and for liquefaction of starch

XX Sequence 498 AA;

Query Match 100.0%; Score 2684; DB 4; Length 498;
 Best Local Similarity 100.0%; Pred. No. 3e-226;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAWWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGGSTTATCNADQKCGG 60
 DB 1 MVAWWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGGSTTATCNADQKCGG 60
 QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTQQLPQTAYGDYHGYWQDIYSLNENYGTADDL 120
 DB 61 TWQGIIDKLDYIQGMGFTAIWITPVTQQLPQTAYGDYHGYWQDIYSLNENYGTADDL 120
 QY 121 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
 DB 121 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
 QY 181 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPVGN 240
 DB 181 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPVGN 240
 QY 241 KAAGYVCIGEVLDGDPATYCPYQNVMDGVNLNPIYIYPLNAPKSTSGSMDDLNNINTVK 300
 DB 241 KAAGYVCIGEVLDGDPATYCPYQNVMDGVNLNPIYIYPLNAPKSTSGSMDDLNNINTVK 300
 QY 301 SDPCDSTLLGTFVENHNDNPRFASVTNDIALAKNVAAFIILNDGPIIYAGQEHYAGGND 360
 DB 301 SDPCDSTLLGTFVENHNDNPRFASVTNDIALAKNVAAFIILNDGPIIYAGQEHYAGGND 360
 QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRGT 420
 DB 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRGT 420
 QY 421 DGSQIVTILSNKGASGDSYTLISLGSAGYTAGQQLTEVIGCTTIVTGVSDGNVPVPMAGGLP 480
 DB 421 DGSQIVTILSNKGASGDSYTLISLGSAGYTAGQQLTEVIGCTTIVTGVSDGNVPVPMAGGLP 480
 QY 481 RVLYPTEKLAGSKICSSS 498
 DB 481 RVLYPTEKLAGSKICSSS 498

RESULT 2

ADT89628
 ID ADT89628 standard; protein; 499 AA.

XX AC ADT89628;

XX DT 16-DEC-2004 (first entry)

XX DE Aspergillus niger neutral alpha-amylase B (amyB) protein.

XX KW Glucoamylase; glaa; amyB; alpha-amylase B; enzyme.

XX OS Aspergillus niger.

XX FN US2004191864-A1.

XX PD 30-SEP-2004.

XX PF 31-MAR-2004; 2004US-00815495.

XX PR 31-MAR-2003; 2003US-0459902P.

XX PA (NOVO) NOVOZYMES BIOTECH INC.

XX PI Connelly M, Brody H;

DR WPI: 2004-708545/69.

DR N-PSDB; ADT89627.

XX PT Producing heterologous biological substance comprises culturing mutant of
 wild-type Aspergillus niger strain in medium suitable for producing
 heterologous biological substance and recovering heterologous biological
 substance.

XX PS Example 10; SEQ ID NO 19; 58pp; English.

XX CC The present invention relates to a method of producing heterologous
 biological substance. The method involves culturing mutant of wild-type
 Aspergillus niger strain in medium suitable for producing heterologous
 biological substance, where mutant strain comprises first nucleotide
 sequence encoding heterologous biological substance and second nucleotide
 sequence comprising modification of glucoamylase (glaA) and recovering
 heterologous biological substance. The present sequence is the
 Aspergillus niger neutral alpha-amylase B (amyB) protein.

XX SQ Sequence 499 AA;

Query Match 99.6%; Score 2674; DB 8; Length 499;
 Best Local Similarity 99.6%; Pred. No. 2.3e-225;
 Matches 496; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MVAWWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGGSTTATCNADQKCGG 60
 DB 2 MVAWWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGGSTTATCNADQKCGG 61
 QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTQQLPQTAYGDYHGYWQDIYSLNENYGTADDL 120
 DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTQQLPQTAYGDYHGYWQDIYSLNENYGTADDL 121
 QY 121 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
 DB 122 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181
 QY 181 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPVGN 240
 DB 182 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPVGN 241
 QY 241 KAAGYVCIGEVLDGDPATYCPYQNVMDGVNLNPIYIYPLNAPKSTSGSMDDLNNINTVK 300
 DB 242 KAAGYVCIGEVLDGDPATYCPYQNVMDGVNLNPIYIYPLNAPKSTSGSMDDLNNINTVK 301
 QY 301 SDPCDSTLLGTFVENHNDNPRFASVTNDIALAKNVAAFIILNDGPIIYAGQEHYAGGND 360
 DB 302 SDPCDSTLLGTFVENHNDNPRFASVTNDIALAKNVAAFIILNDGPIIYAGQEHYAGGND 361
 QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRGT 420
 DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRGT 421
 QY 421 DGSQIVTILSNKGASGDSYTLISLGSAGYTAGQQLTEVIGCTTIVTGVSDGNVPVPMAGGLP 480
 DB 422 DGSQIVTILSNKGASGDSYTLISLGSAGYTAGQQLTEVIGCTTIVTGVSDGNVPVPMAGGLP 481
 QY 481 RVLYPTEKLAGSKICSSS 498
 DB 482 RVLYPTEKLAGSKICSSS 499

RESULT 3

ADT89632
 ID ADT89632 standard; protein; 498 AA.

XX AC ADT89632;

XX DT 16-DEC-2004 (first entry)

XX DE Aspergillus niger neutral alpha-amylase A (amyA) protein.

XX KW Glucoamylase; glaa; amyA; alpha-amylase A; enzyme.

XX OS Aspergillus niger.
XX PN US2004191864-A1.
XX PD 30-SEP-2004.
XX PF 31-MAR-2004; 2004US-00815495.
XX PR 31-MAR-2003; 2003US-0459902P.
XX PA (NOVO) NOVOZYMES BIOTECH INC.
XX PI Connelly M, Brody H;
XX WPI; 2004-708545/69.
XX DR N-PSDB; AD789631.
XX PT Producing heterologous biological substance comprises culturing mutant of
PT wild-type Aspergillus niger strain in medium suitable for producing
PT heterologous biological substance and recovering heterologous biological
PT substance.
XX PS Example 11; SEQ ID NO 22; 58pp; English.
XX CC The present invention relates to a method of producing heterologous
CC biological substance. The method involves culturing mutant of wild-type
CC Aspergillus niger strain in medium suitable for producing heterologous
CC biological substance, where mutant strain comprises first nucleotide
CC sequence encoding heterologous biological substance and second nucleotide
CC sequences comprising modification of glucoamylase (glax) and recovering
CC heterologous biological substance. The present sequence is the
CC Aspergillus niger neutral alpha-amylase A (amyA) protein.
XX SQ Sequence 498 AA;

Query Match 99.2%; Score 2662; DB 8; Length 498;
Best Local Similarity 99.6%; Pred. No. 2.6e-224;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MVAWNSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGTATCNTADOKYCGG 60
DB 2 MVAWNSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGTATCNTADOKYCGG 61

QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTALPQTAYGDYHGYWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTALPQTAYGDYHGYWQDIYSLNENYGTADDL 121

QY 121 KALSSALHERGMYLVVDVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTQ 180
DB 122 KALSSALHERGMYLVVDVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTQ 181

QY 181 VEDCWLGDNTVSLPDLDTTKDVVKNWYDMVGLSVNSYIDGLRIDTVKHQKDFWPGYN 240
DB 182 VEDCWLGDNTVSLPDLDTTKDVVKNWYDMVGLSVNSYIDGLRIDTVKHQKDFWPGYN 241

QY 241 KAAGVYICIGEVLDGDPAYTCPYQNVMDGVLNPIYIYPLNAPKSTSGSMDDLNNMINTVK 300
DB 242 KAAGVYICIGEVLDGDPAYTCPYQNVMDGVLNPIYIYPLNAPKSTSGSMDDLNNMINTVK 301

QY 301 SDCPSTLLGTFFVENHNDPRFASYTNDIALAKNVAFAIILNDGIPIIYAGQCHYAGND 360
DB 302 SDCPSTLLGTFFVENHNDPRFASYTNDIALAKNVAFAIILNDGIPIIYAGQCHYAGND 361

QY 361 PANREATWLSGYPTDSELYKLASANAIRNYAISKDTGPTVYKNMPIYKDDTTIARKGT 420
DB 362 PANREATWLSGYPTDSELYKLASANAIRNYAISKDTGPTVYKNMPIYKDDTTIARKGT 421

QY 421 DGSQIVTILSNKASGSDSYTSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 480
DB 422 DGSQIVTILSNKASGSDSYTSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 481

QY 481 RVLYPEKLAGSKIC 495

DB 482 RVLYPEKLAGSKIC 496

RESULT 4
AAR72450
ID AAR72450 standard; protein; 478 AA.
XX AC AAR72450;
XX DT 25-MAR-2003 (revised)
XX DT 01-DEC-1995 (first entry)
XX DE Aspergillus oryzae alpha amylase (mature protein).
XX KW Alpha amylase; variant; enzyme; detergent; additive; dishwashing;
KW washing; Bacillus licheniformis; Bacillus amyloliquefaciens;
KW Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
KW thermostable.
XX OS Aspergillus oryzae.
XX PN WO9510603-A1.
XX PD 20-APR-1995.
XX PF 05-OCT-1994; 94WO-DK000370.
XX PR 08-OCT-1993; 93DK-00001133.
XX PR 02-FEB-1994; 94DK-00000140.
XX PA (NOVO) NOVO-NORDISK AS.
XX PI Borchert TV, Bisgard-Frantzen H, Svendsen A, Theillersens M;
PI Van Der Zee P;
XX WPI; 1995-161790/21.
XX PT New Bacillus derived alpha-amylase variants - having amino acid
PT modifications to improve washing and/or dishwashing performance.
XX PS Disclosure; Page 75-76; 105pp; English.
XX CC Variant alpha amylase enzymes which have improved washing and/or as
CC detergent additives. The enzymes have one or more amino acid residues
CC added, deleted or substituted. The variants can also be used for textile
CC desizing prior to scouring, bleaching and dyeing. The variants have
CC improved thermostability, acid/alkaline stability; low temperature
CC optimum; pH optimum; higher hydrolysis velocity and improved tolerance to
CC other composition constituents, e.g. oxidation agents. (Updated on 25-MAR
CC -2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 478 AA;

Query Match 95.8%; Score 2572; DB 2; Length 478;
Best Local Similarity 99.8%; Pred. No. 1.9e-216;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPDWRSSQSIYFLLTDRFARTDGTATCNTADOKYCGTWQGIIDKLDYIQGMGFTAI 80
DB 1 ATPDWRSSQSIYFLLTDRFARTDGTATCNTADOKYCGTWQGIIDKLDYIQGMGFTAI 60

QY 81 WITPVTALPQTAYGDYHGYWQDIYSLNENYGTADDLKALSSALHERGMYLVVDVVA 140
DB 61 WITPVTALPQTAYGDYHGYWQDIYSLNENYGTADDLKALSSALHERGMYLVVDVVA 120

QY 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTQVEDCWLGDNTVSLPDLDTTK 200
DB 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTQVEDCWLGDNTVSLPDLDTTK 180

QY 201 DVVKNWYDMVGLSVNSYIDGLRIDTVKHQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
DB 181 DVVKNWYDMVGLSVNSYIDGLRIDTVKHQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240

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QY 261 PYQVMDGVLNPIYYPLLNAPKSTSGSMDDLNNMINTVKSQPCDPTLLGTFVFNHNDNR 320
Db 241 PYQVMDGVLNPIYYPLLNAPKSTSGSMDDLNNMINTVKSQPCDPTLLGTFVFNHNDNR 300

QY 321 FASYTNDIALAKNVAAFIILNDGPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360

QY 381 LIASANAIRNYAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSVT 440
Db 361 LIASANAIRNYAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSVT 420

QY 441 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 498
Db 421 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 5
AAR78270
ID AAR78270 standard; protein; 478 AA.
XX
AC AAR78270;
XX
DT 17-JAN-1996 (first entry)
XX
DE Aspergillus oryzae alpha amylase (mature protein).
XX
KW Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch;
KW thermostable; methionine; Bacillus licheniformis;
KW Bacillus amyloliquefaciens; Bacillus stearothermophilus;
KW Aspergillus oryzae.
XX
OS Aspergillus oryzae.
XX
FN WO9521247-A1.
XX
PD 10-AUG-1995.
XX
PF 05-OCT-1994; 94WO-DK000371.
XX
PR 02-FEB-1994; 94DK-00000141.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Toft AH, Marcher D, Pedersen HH, Nilsson TE;
XX
DR WPI; 1995-283767/37.
XX
PT Use of an oxidation stable alpha-amylase - for simultaneous desizing and
PT bleaching or scouring of fabrics contg. starch or starch derivs.
XX
PS Disclosure; Page 25-26; 37pp; English.
XX
CC Oxidation stable alpha amylases can be used for the simultaneous desizing
CC and bleaching or scouring of a fabric comprising starch or starch
CC derivatives. They exhibit a better heat stability, especially in the
CC presence of oxidising agents. They are obtained from a parent alpha
CC amylase by replacing one or more methionine residues with any amino acid
CC different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or
CC Asp. The parent alpha amylase is pref. derived from a Bacillus species,
CC although alpha amylases of fungal origin can also be used. This sequence
CC is the wild type (unmodified) alpha amylase of Aspergillus oryzae
XX
XX Sequence 478 AA;
XX
Query Match 95.8%; Score 2572; DB 2; Length 478;
Best Local Similarity 99.8%; Pred. No. 1.9e-216;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGTSTTATCNTADQKYCGGTWQGIIDKLDYIQMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRFARTDGTSTTATCNTADQKYCGGTWQGIIDKLDYIQMGFTAI 60

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QY 81 WITPVTALPOTTAYGDAYHGYWQODIYSLNENYCTADDLKALSSALHERGMYLMVDVVA 140
Db 61 WITPVTALPOTTAYGDAYHGYWQODIYSLNENYCTADDLKALSSALHERGMYLMVDVVA 120

QY 141 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFQNYEDQTVQEDCWLGONTVSLPDLDTTK 200
Db 121 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFQNYEDQTVQEDCWLGONTVSLPDLDTTK 180

QY 201 DVVKNEWYDWVGSLSVSNYSIDGLRIDTVKHQKQFPGYNKAAAGVYCI GEVLDDGDPAYTC 260
Db 181 DVVKNEWYDWVGSLSVSNYSIDGLRIDTVKHQKQFPGYNKAAAGVYCI GEVLDDGDPAYTC 240

QY 261 PYQVMDGVLNPIYYPLLNAPKSTSGSMDDLNNMINTVKSQPCDPTLLGTFVFNHNDNR 320
Db 241 PYQVMDGVLNPIYYPLLNAPKSTSGSMDDLNNMINTVKSQPCDPTLLGTFVFNHNDNR 300

QY 321 FASYTNDIALAKNVAAFIILNDGPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360

QY 381 LIASANAIRNYAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSVT 440
Db 361 LIASANAIRNYAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSVT 420

QY 441 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 498
Db 421 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 6
AAW14500
ID AAW14500 standard; protein; 478 AA.
XX
AC AAW14500;
XX
DT 04-JUN-1997 (first entry)
XX
DE Aspergillus oryzae alpha-amylase (mature protein).
XX
KW alpha-amylase; mature; Bacillus licheniformis; termamyl; fungamyl;
KW Aspergillus oryzae; Bacillus amyloliquefaciens; altered property;
KW calcium dependency; substrate binding; stability; pH optimum;
KW thermostability; cleavage; oligosaccharide substrate; dishwashing;
KW washing; detergent additive; fabric desizing; starch liquefaction;
KW sweetener; ethanol production; variant.
XX
OS Aspergillus oryzae.
XX
FH Key Location/Qualifiers
FT Misc-difference 13..45
FT /label= loop 1 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 7-23 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 33"
FT Misc-difference 14..40
FT /label= loop 1 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 8-18 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 35"
FT Misc-difference 28..42
FT /label= loop 1 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 12-19 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 30"
FT Misc-difference 32..38
FT /label= loop 1 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for

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AC ABP96630;
XX 02-JUN-2003 (first entry)
XX Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45.
DE Self-processing plant; plant; processing enzyme; alpha-amylase; grain;
KW pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase;
KW mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch;
KW maltodextrin; ethanol; fermentation; beverage; enzyme.
XX
OS Aspergillus shirousami.
OS Synthetic.
XX WO2003018766-A2.
XX 06-MAR-2003.
XX 27-AUG-2002; 2002WO-US027129.
XX 27-AUG-2001; 2001US-0315281P.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Lanahan MB, Basu SS, Battie CJ, Chen W, Craig J, Kinkema M;
PI WPI; 2003-268420/26.
DR N-PSDB; ACC44572.
XX
XX Novel polynucleotide encoding hyperthermophilic processing enzymes e.g.
PT alpha-amylase, useful for producing plant to produce food products having
PT improved taste or fermentable substrates for ethanol.
XX
PS Claim 1; Page 107; 158pp; English.
XX
CC The present invention describes polynucleotides which encode processing
CC enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose
CC isomerase, or glucoamylase) that are optimised for expression in plants.
CC The polynucleotides encode mesophilic, thermophilic or hyperthermophilic
CC processing enzymes, which are activated under suitable conditions to act
CC upon the desired substrate. Also described are self-processing transgenic
CC plants and plant parts, e.g. grain, which express one or more of these
CC enzymes and have an altered composition that facilitates plant and grain
CC processing. Also described is a method (M) for converting starch to
CC starch-derived products in a transformed plant part (TPP), by activating
CC the starch processing enzyme contained in it. Transgenic grain is useful
CC for preparing maltodextrin. A transformed plant (TP) can be used to
CC produce food products having improved taste and to produce fermentable
CC substrates for ethanol and fermented beverages. (M) eliminates the need
CC to mill or physically disrupt the integrity of plant parts prior to
CC recovery of starch-derived products. The present sequence represents
CC alpha-amylase/glucoamylase fusion protein, which is given in the
CC exemplification of the present invention
XX
SQ Sequence 1095 AA;
Query Match 95.7%; Score 2569; DB 6; Length 1095;
Best Local Similarity 99.8%; Pred. No. 1.3e-215;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 ATPDWRQSIFLLTDFARTDGTTCNTADQKCGTGWQGIIDKLDYIQMGFTAI 80
DB 1 ATPDWRQSIFLLTDFARTDGTTCNTADQKCGTGWQGIIDKLDYIQMGFTAI 60
QY 81 WITPVTALPQTAYGDYHGYWQDIYSLNENYGTADDLKALSALHERGMYLMDVVA 140
DB 61 WITPVTALPQTAYGDYHGYWQDIYSLNENYGTADDLKALSALHERGMYLMDVVA 120
QY 141 NHMGYDGGAGSSVDYSVFPPSSQDYFHPFCFQNYEDQTOVEDCWLGNTVSLPLDITTK 200
DB 121 NHMGYDGGAGSSVDYSVFPPSSQDYFHPFCFQNYEDQTOVEDCWLGNTVSLPLDITTK 180
QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 260

DB 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 240
QY 261 PYQNVMDGLNYPYIYPLLNAPKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHDNPR 320
DB 241 PYQNVMDGLNYPYIYPLLNAPKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHDNPR 300
QY 321 FASVTNDIALAKNVAAFIILNDGPIIYAGOEQHYAGGNDPANREATWLSGVTDSLEYK 380
DB 301 FASVTNDIALAKNVAAFIILNDGPIIYAGOEQHYAGGNDPANREATWLSGVTDSLEYK 360
QY 381 LIASANAIRNYAISKDTGFTYKWPYIKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 440
DB 361 LIASANAIRNYAISKDTGFTYKWPYIKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 420
QY 441 LSLSGAGYTACQQLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 498
DB 421 LSLSGAGYTACQQLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 478
RESULT 8
AAR46065
ID AAR46065 standard; protein; 478 AA.
XX AC AAR46065;
XX 25-MAR-2003 (revised)
DT 18-JUL-1994 (first entry)
XX
DE Mutant alpha-amylase.
XX Methionine substitution; stability; activity; detergent;
KW dishwashing agents; liquifaction agents.
XX
OS Aspergillus oryzae.
XX WO9402597-A1.
XX 03-FEB-1994.
XX 06-JUL-1993; 93WO-DK000230.
XX 23-JUL-1992; 92DK-00000946.
PR 16-DEC-1992; 92DK-00001503.
PR 15-MAR-1993; 93DK-00000292.
XX (NOVO) NOVO-NORDISK AS.
XX Svendsen A, Bisgard-Frantzen H;
WPI; 1994-048855/06.
XX
PT Mutant alpha-amylase from Bacillus species comprising a methionine
PT substitution - with improved stability and activity at low pH, for use in
PT detergents, dishwashing agents and liquifaction agents.
XX
PS Claim 1; Page 7; 20pp; English.
XX
CC The sequence os that of the Ascoerigillus oryzae alpha amylase, sold
CC commercially as FUNGAMYL (TM) by Novo Nordisk A/S. The sequence can be
CC mutated by substitution of one or more of its methionine residues for any
CC amino acid other than cysteine. The mutant alpha-amylase exhibits a
CC better activity level and better stability in the presence of oxidising
CC agents than previous mutant alpha amylases, and improved thermostability
CC at moderately low pH. The enzyme can be used as an additive for
CC detergents, dishwashing agents and liquifaction agents. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
SQ Sequence 478 AA;
Query Match 95.1%; Score 2552; DB 2; Length 478;
Best Local Similarity 99.4%; Pred. No. 1.1e-214;
Matches 475; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	21	ATPADWRSQS	IYFLLTDRPARTDGS	TTATCTNTADQK	YCGGTWQGI	IKDLDYIQGMGFTAI	80	
Db	1	ATPADWRSQS	IYFLLTDRPARTDGS	TTATCTNTADQK	YCGGTWQGI	IKDLDYIQGMGFTAI	60	
Qy	81	WITPVTAQLPQT	TAYGDAYHG	WQODIYSL	ENYGTADDKAL	SSALHERGYMLMDVVA	140	
Db	61	WITPVTAQLPQT	TAYGDAYHG	WQODIYSL	ENYGTADDKAL	SSALHERGYMLMDVVA	120	
Qy	141	NHMGYD	GAGSSVDYSVFKP	PSODYFHP	PCFTONYEDOT	OVEDCWLGN	TWLSLPDLDTTK	200
Db	121	NHMGYD	GAGSSVDYSVFKP	PSODYFHP	PCFTONYEDQ	TGVBCDQ	LGNVTWLSLPDLDTTK	180
Qy	201	DVVKNEWYD	WVGS	LVSNYS	IDGLRIDTVKH	VQKQFWP	GYNKAAGYVCIGEVLDGDPAYTC	260
Db	181	DVVKNEWYD	WVGS	LVSNYS	IDGLRIDTVKH	VQKQFWP	GYNKAAGYVCIGEVLDGDPAYTC	240
Qy	261	PYQNM	DGVLNPIY	YPLNNAFK	STSGMDDL	YNMINTVKS	CDPDLTLLGTVEVHNDR	320
Db	241	PYQNM	DGVLNPIY	YPLNNAFK	STSGMDDL	YNMINTVKS	CDPDLTLLGTVEVHNDR	300
Qy	321	FASYTNDIAL	AKNVA	AIILNDG	PIIYAGOEQ	HYAGNDPAN	REATWLSGYPTDSELYK	380
Db	301	FASYTNDIAL	AKNVA	AIILNDG	PIIYAGOEQ	HYAGNDPAN	REATWLSGYPTDSELYK	360
Qy	381	LIASANAIR	NYAI	SKDTG	FVTVK	WPIYKDDTTI	AMRKGTGDSQIVTILSNKAGSDSYT	440
Db	361	LIASANAIR	NYAI	SKDTG	FVTVK	WPIYKDDTTI	AMRKGTGDSQIVTILSNKAGSDSYT	420
Qy	441	LSLSGAGY	TAGQOLTE	VIGCTT	VTVGSDGN	VPMAGGLPR	VLYPTEKLAGSKI	498
Db	421	LSLSGAGY	TAGQOLTE	VIGCTT	VTVGSDGN	VPMAGGLPR	VLYPTEKLAGSKI	478

RESULT 9	
AAR79025	
ID	AAR79025 standard; protein; 478 AA.
XX	
XX	AAR79025;
XX	
XX	22-MAR-1996 (first entry)
DT	
XX	Mature taka-amylase A.
XX	
XX	Wild type; neopullulanase; B. stearothermophilus; mutant; food industry;
KW	modification; hydrophobicity; replacement insertion; deletion.
XX	
XX	Aspergillus oryzae.
OS	
XX	
XX	Key Location/Qualifiers
FH	
FT	Disulfide-bond 30..38
FT	Disulfide-bond 150..164
FT	Disulfide-bond 240..283
FT	Disulfide-bond 439..474
XX	
XX	JP07177891-A.
PN	
XX	
XX	18-JUL-1995.
PD	
XX	
XX	31-OCT-1994; 94JP-00288658.
PF	
XX	
XX	12-NOV-1993; 93JP-00306096.
PR	
XX	
XX	(NIDE) NEC CORP.
PA	
PA	(EZAK) EZAKI GLICO CO.
XX	
XX	WPI; 1995-279919/37.
DR	
XX	
XX	Modifying a transferase by enhancing hydrophobicity of a selected site -
PT	increases transfer activity, also new mutant neo-pullulanase(s).
PT	
XX	
XX	Disclosure; Page 10-11; 18pp; English.
PS	
XX	

CC	This sequence represents the mature form of taka-amylase from <i>A. oryzae</i> .									
CC	This sequence was used in a method for the generation of mutant									
CC	pullulanases for use in the food industry (see also AAR79026-28). The									
CC	wild type pullulanase enzyme was modified by the method of the invention									
CC	for enhancing the hydrophobicity of a selected site of the pullulanase.									
CC	The method comprises replacement of a group in the selected site with a									
CC	hydrophobic group, replacement of an amino acid with a hydrophobic amino									
CC	acid, and/or insertion or deletion of a hydrophobic amino acid from the									
CC	selected site. The method was used to produce neopullulanases Y377F,									
CC	S422V and M375L									
XX										
SQ	Sequence 478 AA;									
	Query Match	93.3%	Score	2503.5;	DB 2;	Length	478;			
	Best Local Similarity	97.9%;	Pred. No.	2e-210;						
	Matches	468;	Conservative	1;	Mismatches	8;	Indels	1;	Gaps	1;
QY	21	ATPADWRSOSIYELLTDRFARTDGS	TATCNTADQKYCGGTWOGI	IKDKLDYIOGMGFTAI	80					
DB	1	ATPADWRSOSIYELLTDRFARTDGS	TATCNTADQKYCGGTWOGI	IKDKLDYIOGMGFTAI	60					
QY	81	WITPVTQAQLPQTAYGDAVHYGQQDI	YSLNENYGTADDL	KALSSALHERGMVLMVDVVA	140					
DB	61	WITPVTQAQLPQDCAYGDAYTYGWT	DIYSLNENYGTADDL	KALSSALHERGMVLMVDVVA	120					
QY	141	NHMGYDGAGSSVDYSVFKPFSSQDY	FHPFCFIQNYEDQTQVEDCWLGDNT	VSPLDLDTTK	200					
DB	121	NHMGYDGAGSSVDYSVFKPFSSQDY	FHPFCFIQNYEDQTQVEDCWLGDNT	VSPLDLDTTK	180					
QY	201	DVYKNWYDWGSLVNSYIDGLRIDTV	KHVQKDFWPGYKKAAGVYCI	GEVLGDGPAYTC	260					
DB	181	DVYKNWYDWGSLVNSYIDGLRIDTV	KHVQKDFWPGYKKAAGVYCI	GEVLGDGPAYTC	240					
QY	261	PYQNVMDGVLNYPITYPLLNAPKST	SGSMDLLNMLNTVKSDCPDSTLL	CTGFVENHDNPR	320					
DB	241	PYQNVMDGVLNYPITYPLLNAPKST	SGSMDLLNMLNTVKSDCPDSTLL	CTGFVENHDNPR	300					
QY	321	FASYTNDIALAKNVAAFIILNDGIP	IITYAGQEQHYAGGNDPANREAT	WLSGYPTDSLYK	380					
DB	301	FASYTNDIALAKNVAAFIILNDGIP	IITYAGQEQHYAGGNDPANREAT	WLSGYPTDSLYK	360					
QY	381	LIASANAIRNAYISKDTGFVYKNPI	YKDDTTIAMRKGTGDSQIVTIL	SNKSGASGDSYT	440					
DB	361	LIASANAIRNAYISKDTGFVYKN-	PYIKDDTTIAMRKGTGDSQIVTIL	SNKSGASGDSYT	419					
QY	441	LSLSGASYTAGQQLTEVIGCTT	VTGSDGNVPVPMAGGLPRVLY	PTEKLAGSKICSS	498					
DB	420	LSLSGASYTAGQQLTEVIGCTT	VTGSDGNVPVPMAGGLPRVLY	PTEKLAGSKICSDS	477					
RESULT 10										
ABB09072										
ID	ABB09072 standard; protein; 423 AA.									
XX										
AC	ABB09072;									
XX										
DT	26-JUN-2002 (first entry)									
XX										
DE	Aspergillus oryzae TAKA protein (TAA).									
XX										
KW	Thermus sp. IM6501; maltogenic amylase; EC 3.2.1.133; crystallisation;									
KW	protein co-ordinate data; 3 dimensional structure.									
XX										
OS	Aspergillus oryzae.									
XX										
PN	KR2001027418-A.									
XX										
PD	06-APR-2001.									
XX										
PF	09-SEP-1999; 99KE-00039130.									
XX										
PR	09-SEP-1999; 99KE-00039130.									
XX										

PA	(POST-) POSTECH FOUND.	ABB80177	ID	ABB80177 standard; protein; 495 AA.
PA	(SAMY-) SAMYANG GENEX CORP.	XX	AC	ABB80177;
PI	Kim TJ, Park GH;	XX	DT	11-AUG-2003 (first entry)
PI		XX	DE	A. fumigatus AfaAL1.
DR	WPI; 2001-534477/59.	XX	KW	Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase; beta-galactosidase; invertase; lipase; alpha-amylase; laccase; polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose; glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose; glyceride; starch; maltodextrin; oxidated phenolic compound; polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage; textile; tea liquor; cleaning ability.
XX	Manufacturing maltogenic amylase having improved transglycosylation activity, comprises using crystallization.	XX	OS	Aspergillus fumigatus.
PS	Disclosure; Page 188; 196pp; Korean.	XX	PN	WO2003012071-A2.
XX	The present invention describes manufacturing maltogenic amylase (EC 3.2.1.133) having improved transglycosylation activity, comprising using crystallization and the three dimensional structure of maltogenic amylase. Manufacturing maltogenic amylase comprises the following steps: (i) obtaining a gene of maltogenic amylase from Thermus sp. IM6501 (KCTC 5027BP) and inserting the gene into plasmid pUC119 to construct recombinant DNA (pThMA119); (ii) inserting the recombinant DNA to Escherichia coli MC1061, which is cultivated at 37 plus degrees Celsius for 10 hours in Luria-Bertani (LB) media and centrifuging the media to obtain a microbial cell; (iii) suspending the microbial cell with buffer solution at pH 7.5 and obtaining supernatant; and (iv) passing the supernatant through column chromatography and obtaining purified maltogenic amylase. The maltogenic amylase is a dimer comprised of two maltogenic amylase molecules, and a Thermus sp. IM6501 maltogenic amylase (ThMA) crystal. The amylase has a structure containing an activated region that consists of amino acid residues of Asp-328, Glu-357, Asp-424, and a pocket with glucose bound that consists of amino acid residues of Pro44, Tyr45, Arg81, Arg83, Pro118, Cys116, Asn131, Glu132, Val1329, and His1360. The present sequence represents Aspergillus oryzae TAKA protein (TAA), given in comparison with ThMA in the present invention	XX	PD	13-FEB-2003.
XX	Sequence 423 AA;	XX	PF	05-AUG-2002; 2002WO-US024842.
QY	Query Match 80.1%; Score 2151; DB 4; Length 423;	XX	PR	03-AUG-2001; 2001US-0309870P.
Db	Best Local Similarity 95.7%; Pred. No. 1.4e-179;	XX	PA	(ELIT-) ELITRA PHARM INC.
Matches 405; Conservative 2; Mismatches 16; Indels 0; Gaps 0;		XX	PI	Jiang B, Storms R, Roemer T, Bussey H;
QY	25 DWRSSLYFLTDRTARTDGTATCNTADQKCGGTWQGIIDKLDYIQGWFYAIWITP 84	XX	PI	WPI; 2003-332729/31.
Db	1 DWRSSLYFLTDRTARTDGTATCNTADQKCGGTWQGIIDKLDYIQGWFYAIWITP 60	XX	DR	N-PSDB; ABQ80345, ABQ80346.
QY	85 VTAQLPQTAYGDVYGHYQWQDIYSLNENYGTADDLKALSSALHBERGMYLMDVVANHMG 144	XX	PT	Novel isolated Aspergillus fumigatus polypeptide, useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents.
Db	61 VTAQLPQTAYGDVYGHYQWQDIYSLNENYGTADDLKALSSALHBERGMYLMDVVANHMG 120	XX	PS	Claim 17; Page 134-35; 169pp; English.
QY	145 YDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNTVSLPDLDTTKDVVK 204	XX	CC	The sequences given in ABB80164-87 show enzymatic proteins derived from A. fumigatus. These proteins display the catalytic activity of an enzyme such as tannase, cellulase, glucose oxidase, glucoamylase, phytase, beta-galactosidase, invertase, lipase, alpha-amylase, laccase, polygalacturonase or xylanase. Compositions comprising the tannase are useful for modulating the amount of compounds that comprise a gallate ester linkage in a composition. Compositions comprising cellulase are useful for modulating the amount of cellulose in a composition. Compositions comprising glucose oxidase are useful for modulating the amount of glucose or oxygen in a composition. Compositions comprising phytase are useful for modulating the amount of myo-inositol phosphates in a composition. Compositions comprising beta-galactosidase are useful for modulating the amount of lactose in a composition. Compositions comprising sucrose or invertase are useful for modulating the amount of sucrose in a composition. Compositions comprising lipase are useful for modulating the amount of glyceride in a composition. Compositions comprising alpha-amylases are useful for modulating the amount of starches or maltodextrins in a composition. Compositions comprising laccase are useful for modulating the amount of oxidated phenolic compounds in a composition. Compositions comprising polygalacturonases are useful for modulating the amount of high or low molecular weight polygalacturonic acid chains in a composition. Compositions comprising xylanases are useful for modulating the amount of xylan or xylo-oligomers in a composition. The A. fumigatus proteins and corresponding DNA's are useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents. The DNA's are useful to express recombinant enzymes for characterization, modification or industrial uses, to compare with the nucleotide sequence of A.fumigatus to identify duplicated genes of paralogs having the same or similar biochemical activity and/or function, to compare with nucleic acid sequence of other related or distant fungal organisms to identify potential orthologous enzyme genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression

XX Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
 KW beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
 KW polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
 KW glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
 KW glyceride; starch; maltodextrin; oxidated phenolic compound;
 KW polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
 KW textile; tea liquor; cleaning ability.

XX Aspergillus fumigatus.
 XX WO2003012071-A2.
 XX 13-FEB-2003.
 XX 05-AUG-2002; 2002WO-US024842.
 XX 03-AUG-2001; 2001US-0309870P.
 XX (ELIT-) ELITRA PHARM INC.
 XX Jiang B, Storms R, Roemer T, Bussey H;
 XX N-PSDB; ABQ80347, ABQ80348.
 XX WPI; 2003-332729/31.
 XX Novel isolated Aspergillus fumigatus polypeptide, useful in various
 PT industries such as those involved in the making of food and feed,
 PT beverages, textiles and detergents.
 XX Claim 17; Page 139-40; 169pp; English.

XX The sequences given in ABB80164-87 show enzymatic proteins derived from
 CC A. fumigatus. These proteins display the catalytic activity of an enzyme
 CC such as tannase, cellulase, glucose oxidase, glucoamylase, phytase, beta-
 CC galactosidases, invertase, lipase, alpha-amylase, laccase,
 CC polygalacturonase or xylanase. Compositions comprising the tannase are
 CC useful for modulating the amount of compounds that comprise a gallate
 CC ester linkage in a composition. Compositions comprising cellulase are
 CC useful for modulating the amount of cellulose in a composition.
 CC Compositions comprising glucose oxidase are useful for modulating the
 CC amount of glucose or oxygen in a composition. Compositions comprising
 CC phytase are useful for modulating the amount of myo-inositol phosphates
 CC in a composition. Compositions comprising beta-galactosidases are useful
 CC for modulating the amount of lactose in a composition. Compositions
 CC comprising sucrose or invertase are useful for modulating the amount of
 CC sucrose in a composition. Compositions comprising lipase are useful for
 CC modulating the amount of glyceride in a composition. Compositions
 CC comprising alpha-amylases are useful for modulating the amount of
 CC starches or maltodextrins in a composition. Compositions comprising
 CC laccase are useful for modulating the amount of oxidated phenolic
 CC compounds in a composition. Compositions comprising polygalacturonases
 CC are useful for modulating the amount of high or low molecular weight
 CC polygalacturonic acid chains in a composition. Compositions comprising
 CC xylanases are useful for modulating the amount of xylan or xylo-oligomers
 CC in a composition. The A. fumigatus proteins and corresponding DNA's are
 CC useful in various industries such as those involved in the making of food
 CC and feed, beverages, textiles and detergents. The DNA's are useful to
 CC express recombinant enzymes for characterization, modification or
 CC industrial uses, to compare with the nucleotide sequence of A. fumigatus
 CC to identify duplicated genes of paralogs having the same or similar
 CC biochemical activity and/or function, to compare with nucleic acid
 CC sequence of other related or distant fungal organisms to identify
 CC potential orthologous enzyme genes, for selecting and making oligomers
 CC for attachment to a nucleic acid array for examination of expression
 CC patterns, and to raise anti-protein antibodies. The polypeptide having
 CC tannase activity increases the yield of tea liquor from tea leaves,
 CC improves the colour, flavour and health benefits of tea products,
 CC particularly an instant tea product. The polypeptide having cellulase
 CC activity enhances cleaning ability of detergent compositions

XX Sequence 630 AA;

Query Match 68.4%; Score 1835; DB 6; Length 630;
 Best Local Similarity 66.8%; Pred. No. 1.4e-151;
 Matches 334; Conservative 59; Mismatches 101; Indels 6; Gaps 2;
 QY 5 WSLFLYGLQVAAPAL-----AATPADMRSSQSIYFLLTDRFARTDGGTTATCNADQKCG 59
 Db 3 WISQFLPLSLCSLLGQAHAALTPAEWSQSIYFLLTDRFGREDNSTTAACDVTQLRYCG 62
 QY 60 GTWQGIIDKLDYIOGMGFTAIWTFPTAQLPQTAYGDAYHYGYWQODIYSLNENYGTADD 119
 Db 63 GSWQGIINHLDIYIOGMGFTAIWTFPTVTEQFVENTGDTSYHYGYWQONTHEVNANYGTAQD 122
 QY 120 LKALSSALHERGMYLMDVDVANHMGYDGAGSSVDYSVFKPSSODYPFHPFCFIONYEQOT 179
 Db 123 LRDLANALHARGMYLMDVDVANHMGYNGAGSNVYGVETPDSATYFHPYCLITDYNQOT 182
 QY 180 QVEDCWLGDNVTSLSPLDLTTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGY 239
 Db 183 AVEDCWLGDTTVSLSPLDLTTSTAVRSIWDVWVKGVLVANSIDGLRIDTVKHVEKDFWPGY 242
 QY 240 NKAAGVYVIGEVLDGDPAYTCYQNVMDGVNLNPIYYPYLLANAFKSTSGSMODLYNMINTV 299
 Db 243 NDAAGVYCVGEVFGDPQYTCYQNYLDGVNLNPIYIYQLYAFPOSTSGISNLNMISSV 302
 QY 300 KSDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPPIYAGQEQHYAGCN 359
 Db 303 ASDCADPTLLGNFTEHNDNPRFASVTSYDSQAKNVISPMFFSDGIPPIYAGQEQHYSGA 362
 QY 360 DPANREATWLSGYPTDSLYKLIASANAIRNAYISKOTGFVYTKNWPYIKDDTTIAMRKG 419
 Db 363 DPANREAVWLSGYSTSATLYSWIASTNKIRLAISKDSAYITSKNPNFYDSTNLAMRKG 422
 QY 420 T-DCSQIVTILSNKSGSDSYTSLSGAGYTAGOOLTEVICGTTVTVGSDGNVPVPMAGG 478
 Db 423 SVAGSQVITVLSNKGSGSYTSLSLSGYTGAGATLVEVMTCTTLTVDSSGNLAVPMVSG 482
 QY 479 LPRVLYPTEKLAGSKICSSS 498
 Db 483 LPRVFPSSWVSGSLCGDS 502

RESULT 14
 AAE24207
 ID AAE24207 standard; protein; 484 AA.
 XX AAE24207;
 AC AAE24207;
 XX 04-OCT-2002 (first entry)
 DT Aspergillus niger alpha-amylase protein.
 DE Ethanol production; starch; fermentation; liquefaction; alpha-amylase;
 KW fuel alcohol; fuel additive; neutral spirit; industrial ethanol; enzyme.
 XX Aspergillus niger.
 PN WO200238787-A2.
 XX 16-MAY-2002.
 PD 09-NOV-2001; 2001WO-DK0000737.
 XX 10-NOV-2000; 2000DK-00001676.
 PR 21-NOV-2000; 2000US-0252213P.
 PR 11-DEC-2000; 2000DK-00001854.
 PR 15-DEC-2000; 2000US-0256015P.
 XX (NOVO) NOVOZYMES AS.
 PA (NOVO) NOVOZYMES NORTH AMERICA INC.
 XX Veit C, Felby C, Fuglsang CC;
 PI WPI; 2002-479793/51.
 DR

XX Producing ethanol from starch-containing material e.g., tubers, roots,
PT whole grain, for use in fuel, by fermentation comprises carrying out a
PT secondary liquefaction step in the presence of a thermostable acid alpha-
PT amylase.
XX
XX
XX Claim 35; Page 31-33; 33pp; English.
XX
XX The invention relates to a method for producing ethanol from starch-
CC containing material, by fermentation. The method involves carrying out a
CC secondary liquefaction step in the presence of a thermostable acid alpha-
CC amylase. The method is used in producing ethanol from a starch-containing
CC material such as tubers, roots or whole grain (e.g. corn, wheat or barley
CC or their combination) or combination of the materials. Preferably ethanol
CC is produced from starch-containing material that is obtained from cereals
CC or from corns, cobs, wheat, barley, rye, milo and potatoes or their
CC combination. The ethanol produced by above mentioned method is used as
CC fuel alcohol and/or fuel additive. The ethanol is also useful as drinking
CC ethanol i.e., potable neutral spirits or industrial ethanol. The present
CC sequence is *Aspergillus niger* alpha-amylase protein
XX
XX Sequence 484 AA;

Query Match 66.2%; Score 1778; DB 5; Length 484;
Best Local Similarity 66.9%; Pred. No. 9.1e-147;
Matches 318; Conservative 63; Mismatches 94; Indels 0; Gaps 0;
QY 24 ADWRQSIVFLLTDRFARTDGTATCNTADQKCGTQWQGIIDKLDYIQGMGFTAIWIT 83
DB 4 ASWRQSIVFLLTDRFRTDNTTATCNTGNEIYCGSGWQGIIDHLDYIEGGMFTAIWIS 63
QY 84 PVTAQLPQTAYGDAGHYGWQDIYSLNENYGTADDLKALSALHARGMYLMDVVVVDH 143
DB 64 PITEQLPQDTADGEAYHGWQKIYDVNSNFTADNLKSLSDALHARGMYLMDVVVVDH 123
QY 144 GYDAGSSVDYSVPKPFSSQDYFHPFCFIONYEDQTOVEDCWLGNTVSLPDLTTKDV 203
DB 124 GYAGNGNDVYSVPDPSSSYFHPYCLITDNDLTMWEDCWEGDTIVSLPDLTTETAV 183
QY 204 KNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICGEVLDDGPAYTCPYQ 263
DB 184 RTIWDVADLVSNYSVDGLRIDSLEVPDPFPFGYNKASGVYCVGEINDGNPASCPCYQ 243
QY 264 NVMDGVNLPIYIPLNAPKSTSGSMDLLYNMINTVKSDCPDSTLLGTVEHNDNPRFAS 323
DB 244 KVLGDVNLPIYIPLNAPKSTSGSMDLLYNMINTVKSDCPDSTLLGTVEHNDNPRFAS 303
QY 324 YNDIALAKNVAFIILNDGPIIYAGQHQHAGGNDPANREATWLSGYPTDSELYKLTIA 383
DB 304 YTSQAKNVLISYIFLSDGPIVYAGEBQHYAGGKVPYNREATWLSGYPTDSELYKLTIA 363
QY 384 SANAIENYAIKSDTGFVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGSGDSTYLSL 443
DB 364 TTNAIRKLAADSAYITVANDAFYDTSNTIAMKGTSGSQVITVLSNKGSGSTYLTLL 423
QY 444 SGAGYTAGOOLTEVICCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
DB 424 SSGYTSKGLIEATCTSVTVDSGDIIPVPMASGLPRVLLPASVVDSSSLCGGS 478

RESULT 15
ADS75939
ID ADS75939 standard; protein; 484 AA.
XX
XX ADS75939;
XX
XX 16-DEC-2004 (first entry)
XX
XX *Aspergillus niger* acid alpha-amylase for ethanol production method.
DE
XX enzyme; alcohol; slurry; water; granular starch; acid alpha-amylase;
KW glucoamylase; gelatinization; yeast; beer; fuel ethanol; potable ethanol;
KW industrial ethanol.

XX *Aspergillus niger*.
XX WO2004080923-A2.
XX
XX 23-SEP-2004.
XX
XX 10-MAR-2004; 2004WO-DK000154.
XX 10-MAR-2003; 2003US-0453326P.
XX (NOVO) NOVOZYMES AS.
XX Olsen HS, Pedersen S, Festersen RM;
XX WPI; 2004-677503/66.
XX Production of alcohol product, e.g. beer, comprises holding slurry of
PT water and granular starch in presence of acid alpha-amylase and
PT glucoamylase followed by simultaneous saccharification and fermentation.
XX
XX Claim 9; SEQ ID NO 1; 43pp; English.
XX
XX The invention relates to a method for the production of an alcohol
CC product by holding a slurry of water and granular starch in the presence
CC of an acid alpha-amylase and a glucoamylase at 0-20 deg C below the
CC initial gelatinization temperature of the granular starch; holding the
CC slurry in the presence of acid alpha-amylase, glucoamylase and yeast at
CC 10-35 deg C to produce ethanol; and optionally recovering the ethanol.
CC The method is used for the production of an alcohol product such as beer
CC or recovered ethanol, e.g. fuel ethanol, potable ethanol or industrial
CC ethanol. This sequence represents an acid fungal alpha-amylase from
CC *Aspergillus niger* used in the method of the invention.
XX
XX Sequence 484 AA;

Query Match 66.2%; Score 1778; DB 8; Length 484;
Best Local Similarity 66.9%; Pred. No. 9.1e-147;
Matches 318; Conservative 63; Mismatches 94; Indels 0; Gaps 0;
QY 24 ADWRQSIVFLLTDRFARTDGTATCNTADQKCGTQWQGIIDKLDYIQGMGFTAIWIT 83
DB 4 ASWRQSIVFLLTDRFRTDNTTATCNTGNEIYCGSGWQGIIDHLDYIEGGMFTAIWIS 63
QY 84 PVTAQLPQTAYGDAGHYGWQDIYSLNENYGTADDLKALSALHARGMYLMDVVVVDH 143
DB 64 PITEQLPQDTADGEAYHGWQKIYDVNSNFTADNLKSLSDALHARGMYLMDVVVVDH 123
QY 144 GYDAGSSVDYSVPKPFSSQDYFHPFCFIONYEDQTOVEDCWLGNTVSLPDLTTKDV 203
DB 124 GYAGNGNDVYSVPDPSSSYFHPYCLITDNDLTMWEDCWEGDTIVSLPDLTTETAV 183
QY 204 KNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICGEVLDDGPAYTCPYQ 263
DB 184 RTIWDVADLVSNYSVDGLRIDSLEVPDPFPFGYNKASGVYCVGEINDGNPASCPCYQ 243
QY 264 NVMDGVNLPIYIPLNAPKSTSGSMDLLYNMINTVKSDCPDSTLLGTVEHNDNPRFAS 323
DB 244 KVLGDVNLPIYIPLNAPKSTSGSMDLLYNMINTVKSDCPDSTLLGTVEHNDNPRFAS 303
QY 324 YNDIALAKNVAFIILNDGPIIYAGQHQHAGGNDPANREATWLSGYPTDSELYKLTIA 383
DB 304 YTSQAKNVLISYIFLSDGPIVYAGEBQHYAGGKVPYNREATWLSGYPTDSELYKLTIA 363
QY 384 SANAIENYAIKSDTGFVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGSGDSTYLSL 443
DB 364 TTNAIRKLAADSAYITVANDAFYDTSNTIAMKGTSGSQVITVLSNKGSGSTYLTLL 423
QY 444 SGAGYTAGOOLTEVICCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
DB 424 SSGYTSKGLIEATCTSVTVDSGDIIPVPMASGLPRVLLPASVVDSSSLCGGS 478

Search completed: November 7, 2005, 18:57:39
Job time : 295.301 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:40:32 ; Search time 57.6834 Seconds
(without alignments)
830.671 Million cell updates/sec

Title: US-10-820-200-2
Perfect score: 2684
Sequence: 1 MVAWWSLFYGLQVAPALAA.....LPRVLYPTEKLAGSKICSSS 498
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: piri:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2684	100.0	499	1 ALAS1	alpha-amylase (EC
2	2675	99.7	499	2 JS0663	alpha-amylase (EC
3	2674	99.6	499	1 ALAS3	alpha-amylase (EC
4	2674	99.6	499	2 B43305	alpha-amylase (EC
5	2673	99.6	499	2 JN0588	alpha-amylase (EC
6	2662	99.2	498	2 A48305	alpha-amylase (EC
7	2656	99.0	499	2 J70466	alpha-amylase (EC
8	2503.5	93.3	478	2 JK0201	alpha-amylase (EC
9	1780	66.3	484	1 A35282	alpha-amylase (EC
10	1629	60.7	624	1 JC4510	pullulanase (EC 3.
11	1527	56.9	507	2 S33921	alpha-amylase (EC
12	1449	54.0	512	2 S06115	alpha-amylase (EC
13	1445.5	53.9	512	2 S23355	alpha-amylase (EC
14	1397.5	52.1	494	1 ALBYAF	alpha-amylase (EC
15	1264	47.1	631	2 S72270	alpha-amylase (EC
16	1015.5	37.8	513	2 T38770	alpha-amylase a pr
17	963.5	35.9	625	2 T41603	alpha-amylase - fi
18	920.5	34.3	491	2 T39448	probable alpha-am
19	899	33.5	581	2 S62505	probable alpha-am
20	898.5	33.5	564	2 T41503	alpha-amylase - fi
21	898	33.5	478	2 T40860	probable alpha-am
22	737	27.5	482	2 S34478	alpha-amylase (EC
23	670	25.0	1196	2 A29130	beta-amylase (EC 3
24	653.5	24.3	774	2 T39539	alpha-amylase homo
25	481.5	17.9	642	2 A11827	cyclomaltodextrin
26	456.5	17.0	713	1 ALBSG1	cyclomaltodextrin
27	454.5	16.9	712	1 ALBSG3	cyclomaltodextrin
28	444.5	16.6	713	1 ALBSG7	cyclomaltodextrin
29	440.5	16.4	528	1 ALBSK	alpha-amylase (EC

ALIGNMENTS

RESULT 1

ALAS1

Alpha-amylase (EC 3.2.1.1) 1 precursor [validated] - Aspergillus oryzae
N:Alternate names: alpha-amylase isozyme II; glycogenase; taka-amylase A
C:Species: Aspergillus oryzae
C:Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
C:Accession: S04548; A33214; JS0240; A91930; A93767; A10627
R:Wirsael, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A:Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon
A:Reference number: S04548; MUID:89237897; PMID:2785629
A:Accession: S04548
A:Molecule type: DNA
A:Residues: 1-499 <WIR>
A:Cross-references: UNIPROT:P10529; EMBL:X12725; NID:g2430; PIDN:CAA31218.1; PID:g295921
A:Genetics: AMY1
A:Accession: A33214
A:Molecule type: mRNA
A:Residues: 1-499 <WI2>
A:Cross-references: GB:X12725; NID:g2430; PIDN:CAA31218.1; PID:g295921
R:Genes, M.J.; Dove, M.J.; Seligy, V.L.
Gene 79, 107-117, 1989

30	433	16.1	710	2	S63598	cyclomaltodextrin
31	428.5	16.0	655	1	ALKBG	cyclomaltodextrin
32	428	15.9	703	1	ALBSX1	cyclomaltodextrin
33	424.5	15.8	919	2	S28179	alpha-amylase (EC
34	418	15.6	713	2	A58800	cyclomaltodextrin
35	418	15.6	714	1	ALBSGR	cyclomaltodextrin
36	414.5	15.4	713	2	S09196	cyclomaltodextrin
37	412	15.4	717	1	S28784	alpha-amylase (EC
38	410	15.3	483	2	G75392	glycosyl hydrolase
39	407	15.2	704	2	I39805	cyclomaltodextrin
40	406.5	15.1	718	1	ALBSGC	cyclomaltodextrin
41	405.5	15.1	718	1	ALBSG6	cyclomaltodextrin
42	405	15.1	713	1	ALBSXR	cyclomaltodextrin
43	399.5	14.9	718	1	ALBSMX	cyclomaltodextrin
44	384.5	14.3	711	1	ALBSXF	cyclomaltodextrin
45	376.5	14.0	1104	2	A60999	alpha-amylase (EC

A:Gene: amy1
A:Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C:Genetics: <AMY2>
A:Gene: amy2; AmyII
A:Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <Sig>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
F:142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
F:218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:227,251,318/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 2684; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 7e-185;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVAWNSFLYGLQVAAPALAAPADWRSSQSIYFLLTDRPARTDGSSTTATCNTADOKYCGG 60
Db 2 MVAWNSFLYGLQVAAPALAAPADWRSSQSIYFLLTDRPARTDGSSTTATCNTADOKYCGG 61

Qy 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVHGYWQODIYSLNENYGTADDL 120
Db 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVHGYWQODIYSLNENYGTADDL 121

Qy 121 KALSSALHERGMVLMVDVVAHMGYDGSVDYSVFKPFSSQDYFHPFCFIONYEDQTQ 180
Db 122 KALSSALHERGMVLMVDVVAHMGYDGSVDYSVFKPFSSQDYFHPFCFIONYEDQTQ 181

Qy 181 VEDCWLGNTVSLPDLDTTKDVVKNWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 240
Db 182 VEDCWLGNTVSLPDLDTTKDVVKNWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 241

Qy 241 KAAGVYCIGEVLDGDPAYTCYQNVMDGLVNPYIYPLNAPFKSTGSMDDLNNINTVK 300
Db 242 KAAGVYCIGEVLDGDPAYTCYQNVMDGLVNPYIYPLNAPFKSTGSMDDLNNINTVK 301

Qy 301 SDCPDSTLLGTFVENHNDPRFASVTNDIALAKNVAAFIILNDGPIIYAGQEHYAGGND 360
Db 302 SDCPDSTLLGTFVENHNDPRFASVTNDIALAKNVAAFIILNDGPIIYAGQEHYAGGND 361

Qy 361 PANREATWLSGYPTDSSELYKLIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRXTG 420
Db 362 PANREATWLSGYPTDSSELYKLIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRXTG 421

Qy 421 DGSQIVTILSNKGASGDSYTLSSGAGYTAGQQLTEVIGCTTIVTGVSGNVVPVMAGGLP 480
Db 422 DGSQIVTILSNKGASGDSYTLSSGAGYTAGQQLTEVIGCTTIVTGVSGNVVPVMAGGLP 481

Qy 481 RVLYPTEKLAGSKICSSS 498
Db 482 RVLYPTEKLAGSKICSSS 499

RESULT 2
JS0663
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus sp.
C:Species: Aspergillus sp.
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
C:Accession: JS0663
R:Shibuya, I.; Tamura, G.; Ishikawa, T.; Hara, S.
Biosci. Biotechnol. Biochem. 56, 174-179, 1992
A:Title: Cloning of the alpha-amylase cDNA of Aspergillus shiroyae and its expression
A:Reference number: JS0663; MUID:92323146; PMID:1368777
A:Accession: JS0663
A:Molecule type: mRNA
A:Residues: 1-499 <SHI>
C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <Sig>
F:22-499/Product: alpha-amylase #status predicted <ALP>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.7%; Score 2675; DB 2; Length 499;
Best Local Similarity 99.8%; Pred. No. 3.1e-184;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVAWNSFLYGLQVAAPALAAPADWRSSQSIYFLLTDRPARTDGSSTTATCNTADOKYCGG 60
Db 2 MVAWNSFLYGLQVAAPALAAPADWRSSQSIYFLLTDRPARTDGSSTTATCNTADOKYCGG 61

Qy 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVHGYWQODIYSLNENYGTADDL 120
Db 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVHGYWQODIYSLNENYGTADDL 121

Qy 121 KALSSALHERGMVLMVDVVAHMGYDGSVDYSVFKPFSSQDYFHPFCFIONYEDQTQ 180
Db 122 KALSSALHERGMVLMVDVVAHMGYDGSVDYSVFKPFSSQDYFHPFCFIONYEDQTQ 181

Qy 181 VEDCWLGNTVSLPDLDTTKDVVKNWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 240
Db 182 VEDCWLGNTVSLPDLDTTKDVVKNWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 241

Qy 241 KAAGVYCIGEVLDGDPAYTCYQNVMDGLVNPYIYPLNAPFKSTGSMDDLNNINTVK 300
Db 242 KAAGVYCIGEVLDGDPAYTCYQNVMDGLVNPYIYPLNAPFKSTGSMDDLNNINTVK 301

Qy 301 SDCPDSTLLGTFVENHNDPRFASVTNDIALAKNVAAFIILNDGPIIYAGQEHYAGGND 360
Db 302 SDCPDSTLLGTFVENHNDPRFASVTNDIALAKNVAAFIILNDGPIIYAGQEHYAGGND 361

Qy 361 PANREATWLSGYPTDSSELYKLIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRXTG 420
Db 362 PANREATWLSGYPTDSSELYKLIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRXTG 421

Qy 421 DGSQIVTILSNKGASGDSYTLSSGAGYTAGQQLTEVIGCTTIVTGVSGNVVPVMAGGLP 480
Db 422 DGSQIVTILSNKGASGDSYTLSSGAGYTAGQQLTEVIGCTTIVTGVSGNVVPVMAGGLP 481

Qy 481 RVLYPTEKLAGSKICSSS 498
Db 482 RVLYPTEKLAGSKICSSS 499

RESULT 3
ALAS3
alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae
N:Alternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A
C:Species: Aspergillus oryzae
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S04549; A33215; A44713
R:Wiesel, S.; Lachmund, A.; Wildhardt, G.; Rutkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A:Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon organization
A:Reference number: S04548; MUID:89237897; PMID:2785629
A:Accession: S04549
A:Molecule type: DNA
A:Residues: 1-499 <WIR>
A:Cross-references: UNIPROT:Q96TH4; EMBL:X12727; NID:G2454; PIDN:CAA31220.1; PID:G295922
A:Accession: A33215
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-499 <WIR>
A:Cross-references: GB:X12727; NID:G2454; PIDN:CAA31220.1; PID:G295922
R:Genes, M.J.; Dove, M.J.; Seligy, V.L.
Gene 79, 107-117, 1989
A:Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing

A:Reference number: JS0240; MUID:89378767; PMID:2789162

A:Accession: A44713

A:Molecule type: DNA

A:Residues: 1-499 <GEN>

A:Note: the authors refer to this as isozyme I

R.Mateuira, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.

J. Biochem. 95, 697-702, 1984

A:Title: Structure and possible catalytic residues of Taka-amylase A.

A:Reference number: A37454; MUID:84212370; PMID:6609921

A:Contents: annotation; X-ray crystallography, 3.0 angstroms

C:Comment: One atom of calcium per molecule is essential for activity.

C:Genetics:

A:Gene: amy3; AmyI

A:Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C:Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; metal

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-499/Product: alpha-amylase 3 #status experimental <MAT>

F:194-321/Domain: alpha-amylase core homology <AMY>

F:51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental

F:142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted

F:218/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:231,251,318/Active site: His, Glu, Asp #status experimental

Query Match 99.6%; Score 2674; DB 1; Length 499;

Best Local Similarity 99.6%; Pred. No. 3.7e-184;

Matches 496; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVANWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGG 60

DB 2 MVANWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGG 61

QY 61 TWQGIIDKLDYIQGMGFTAIWITPTVAQLPQTAYGDVHGYWQDIYSLNENYGTADDL 120

DB 62 TWQGIIDKLDYIQGMGFTAIWITPTVAQLPQTAYGDVHGYWQDIYSLNENYGTADDL 121

QY 121 KALSSALHERGMYLWVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQIQ 180

DB 122 KALSSALHERGMYLWVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQIQ 181

QY 181 VEDCWLGNTVSLPDLDTTKOVVKNWYDVGSLVSNYSIDGLRIDTVKHQKDFWPGYN 240

DB 182 VEDCWLGNTVSLPDLDTTKOVVKNWYDVGSLVSNYSIDGLRIDTVKHQKDFWPGYN 241

QY 241 KAAGVYICGEVLDDGPAYTCPYQNVMDGVLNPIYYPLNNAFKSTSGSMDLLYNMINTVK 300

DB 242 KAAGVYICGEVLDDGPAYTCPYQNVMDGVLNPIYYPLNNAFKSTSGSMDLLYNMINTVK 301

QY 301 SDPCDSTLLGTVEVNDHNPFRFASNTNDIALAKNVAFIILNDGIPIIYAGQEHYAGGND 360

DB 302 SDPCDSTLLGTVEVNDHNPFRFASNTNDIALAKNVAFIILNDGIPIIYAGQEHYAGGND 361

QY 361 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTKNMPYIKDDTTIAMRKGT 420

DB 362 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTKNMPYIKDDTTIAMRKGT 421

QY 421 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 480

DB 422 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 481

QY 481 RVLYPTEKLAGSKICSSS 498

DB 482 RVLYPTEKLAGSKICSSS 499

RESULT 4

B48305

alpha-amylase (EC 3.2.1.1) B precursor - Aspergillus awamori

C:Species: Aspergillus awamori

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C:Accession: B48305

R.Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;

Curr. Genet. 17, 203-212, 1990

A:Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe

A:Reference number: A48305; MUID:90254827; PMID:2340591

A:Accession: B48305

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-499 <KOR>

A:Cross-references: UNIPROT:Q02906

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F:194-321/Domain: alpha-amylase core homology <AMY>

Query Match 99.6%; Score 2674; DB 2; Length 499;

Best Local Similarity 99.6%; Pred. No. 3.7e-184;

Matches 496; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MVANWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGG 60

DB 2 MVANWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGG 61

QY 61 TWQGIIDKLDYIQGMGFTAIWITPTVAQLPQTAYGDVHGYWQDIYSLNENYGTADDL 120

DB 62 TWQGIIDKLDYIQGMGFTAIWITPTVAQLPQTAYGDVHGYWQDIYSLNENYGTADDL 121

QY 121 KALSSALHERGMYLWVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQIQ 180

DB 122 KALSSALHERGMYLWVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQIQ 181

QY 181 VEDCWLGNTVSLPDLDTTKOVVKNWYDVGSLVSNYSIDGLRIDTVKHQKDFWPGYN 240

DB 182 VEDCWLGNTVSLPDLDTTKOVVKNWYDVGSLVSNYSIDGLRIDTVKHQKDFWPGYN 241

QY 241 KAAGVYICGEVLDDGPAYTCPYQNVMDGVLNPIYYPLNNAFKSTSGSMDLLYNMINTVK 300

DB 242 KAAGVYICGEVLDDGPAYTCPYQNVMDGVLNPIYYPLNNAFKSTSGSMDLLYNMINTVK 301

QY 301 SDPCDSTLLGTVEVNDHNPFRFASNTNDIALAKNVAFIILNDGIPIIYAGQEHYAGGND 360

DB 302 SDPCDSTLLGTVEVNDHNPFRFASNTNDIALAKNVAFIILNDGIPIIYAGQEHYAGGND 361

QY 361 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTKNMPYIKDDTTIAMRKGT 420

DB 362 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTKNMPYIKDDTTIAMRKGT 421

QY 421 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 480

DB 422 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 481

QY 481 RVLYPTEKLAGSKICSSS 498

DB 482 RVLYPTEKLAGSKICSSS 499

RESULT 5

JN0588

alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae

N:Alternate names: Taka-amylase A

C:Species: Aspergillus oryzae

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: JN0588

R.Tsukagoshi, N.; Furukawa, M.; Nagaba, H.; Kiritu, N.; Teuboi, A.; Uda, S.

Gene 84, 319-327, 1989

A:Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for m

A:Reference number: JN0588; MUID:90128276; PMID:2612911

A:Accession: JN0588

A:Molecule type: mRNA

A:Residues: 1-499 <TSU>

A:Cross-references: UNIPROT:Q96TH4

C;Comment: The alpha amylases are encoded by multigene family.

C;Genetics:

A;Gene: Taa-G1

A;Introns: 56/1; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-499/Product: alpha-amylase #status predicted <MAT>

F;194-321/Domain: alpha-amylase core homology <AMY>

F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.6%; Score 2673; DB 2; Length 499;
Best Local Similarity 99.6%; Pred. No. 4.3e-184;
Matches 496; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGSSTTATCNTADQKCGG 60
DB 2 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGSSTTATCNTADQKCGG 61
QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTQAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTQAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL 121
QY 121 KALSSALHERGMVLMVDVVAHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
DB 122 KALSSALHERGMVLMVDVVAHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181
QY 181 VEDCWLGNTVSLPDLDTTKDVVKNWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPQYN 240
DB 182 VEDCWLGNTVSLPDLDTTKDVVKNWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPQYN 241
QY 241 KAAGYVCIGEVLGDGPAYTCYQNVMDGVNLNPIYPLNAPKSTSGMDDLNNINTVK 300
DB 242 KAAGYVCIGEVLGDGPAYTCYQNVMDGVNLNPIYPLNAPKSTSGMDDLNNINTVK 301
QY 242 KAAGYVCIGEVLGDGPAYTCYQNVMDGVNLNPIYPLNAPKSTSGMDDLNNINTVK 301
QY 301 SDCPDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPILYAGQEHYAGND 360
DB 302 SDCPDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPILYAGQEHYAGND 361
QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRGT 420
DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRGT 421
QY 421 DGSQVITILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 480
DB 422 DGSQVITILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 481
QY 481 RVLVPTTEKLAGSKICSS 498
DB 482 RVLVPTTEKLAGSKICSS 499

RESULT 6

A48305

alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori

C;Species: Aspergillus awamori

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C;Accession: A48305

R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;

Curr. Genet. 17, 203-212, 1990

A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Asper

A;Reference number: A48305; MUID:90254827; PMID:2340591

A;Accession: A48305

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-498 <KOR>

A;Cross-references: UNIPROT:Q02905

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology <AMY>

Query Match 99.2%; Score 2662; DB 2; Length 498;
Best Local Similarity 99.6%; Pred. No. 2.7e-183;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGSSTTATCNTADQKCGG 60
DB 2 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGSSTTATCNTADQKCGG 61
QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTQAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTQAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL 121
QY 121 KALSSALHERGMVLMVDVVAHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
DB 122 KALSSALHERGMVLMVDVVAHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181
QY 181 VEDCWLGNTVSLPDLDTTKDVVKNWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPQYN 240
DB 182 VEDCWLGNTVSLPDLDTTKDVVKNWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPQYN 241
QY 241 KAAGYVCIGEVLGDGPAYTCYQNVMDGVNLNPIYPLNAPKSTSGMDDLNNINTVK 300
DB 242 KAAGYVCIGEVLGDGPAYTCYQNVMDGVNLNPIYPLNAPKSTSGMDDLNNINTVK 301
QY 301 SDCPDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPILYAGQEHYAGND 360
DB 302 SDCPDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPILYAGQEHYAGND 361
QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRGT 420
DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRGT 421
QY 421 DGSQVITILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 480
DB 422 DGSQVITILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 481
QY 481 RVLVPTTEKLAGSKIC 495
DB 482 RVLVPTTEKLAGSKIC 496

RESULT 7

JT0466

alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae

N;Alternate names: glycogenase; Taka-amylase A

C;Species: Aspergillus oryzae

C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004

C;Accession: JT0466

R;Tada, S.; Iimura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.

Agric. Biol. Chem. 53, 593-599, 1989

A;Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergill

A;Reference number: JT0466

A;Accession: JT0466

A;Molecule type: DNA

A;Residues: 1-499 <AD>

A;Cross-references: UNIPROT:P10529

C;Comment: See also PIR:JK0201 and PIR:JSQ240.

C;Comment: One atom of calcium per molecule is essential for activity.

C;Genetics:

A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-499/Product: alpha-amylase #status predicted <MAT>

F;194-321/Domain: alpha-amylase core homology <AMY>

F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:231,251,318/Active site: His, Glu, Asp #status predicted

Query Match 99.0%; Score 2656; DB 2; Length 499;
Best Local Similarity 99.4%; Pred. No. 7.2e-183;
Matches 495; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	MVAWSFLYGLQVAAPALAAATPADWRSOSIYFLLTDRFARTDGSSTATCNTADQKYCGG	60
DB	2	MVAWSFLYGLQVAAPALAAATPADWRSOSIYFLLTDRFARTDGSSTATCNTADQKYCGG	61
QY	61	TWQGIIDKLDYIOGMGFTAIWTPVTAQPLQTTAYGDVHYGQQDIYSLNENYGTADDL	120
DB	62	TWQGIIDKLDYIOGMGFTAIWTPVTAQPLQTTAYGDVHYGQQDIYSLNENYGTADDL	121
QY	121	KALSSALHGRMYLMDVVDVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQYEDQTO	180
DB	122	KALSSALHGRMYLMDVVDVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQYEDQTO	181
QY	181	VEDCWLGDNVSLPDLDTTKDVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN	240
DB	182	VEYCWLGDNVSLPDLDTTKDVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN	241
QY	241	KAAGVYICIGEVLDGDPAYTCFYQNVMDGVLYPIYPLNAPKSTSGSMDLLYNMINTVK	300
DB	242	KAAGVYICIGEVLDGDPAYTCFYQNVMDGVLYPIYPLNAPKSTSGSMDLLYNMINTVK	301
QY	301	SDCPDSTLLGTFVENHNDNPRFASYTNDIALAKNVAAFIILNDGIPYIYAGQHQHYAGND	360
DB	302	SDCPDSTLLGTFVENHNDNPRFASYTNDIALAKNVAAFIILNDGIPYIYAGQHQHYAGND	361
QY	361	PANREATWLSGYPTDSELYKLATASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT	420
DB	362	PANREATWLSGYPTDSELYKLATASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT	421
QY	421	DGSOIYVILSNKGASGDSYTLISGAGYTAGOOLTEVIGCTTVTVGSDGNVPPVPMAGGLP	480
DB	422	DGSOIYVILSNKGASGDSYTLISGAGYTAGOOLTEVIGCTTVTVGSDGNVPPVPMAGGLP	481
QY	481	RVLYPEKLAGSKICSSS 498	
DB	482	RVLYPEKLAGSKICSSS 499	

RESULT 8
JK0201
alpha-amylase (EC 3.2.1.1) - Aspergillus oryzae
N:Alternate names: glycogenase; Taka-amylase A
C:Species: Aspergillus oryzae
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
R:Toda, H.; Kondo, K.; Narita, K.
Proc. Jpn. Acad. 58B, 208-212, 1982
A:Title: The complete amino acid sequence of Taka-amylase A.
A:Reference number: JK0201
A:Accession: JK0201
A:Molecule type: protein
A:Residues: 1-478 <TOD>
A:Cross-references: UNIPROT:P10529
C:Comment: One atom of calcium per molecule is essential for the activity.
C:Comment: This enzyme is a glycoprotein.
C:Comment: See also PIR:J70466 and PIR:JS0240.
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:173-300/Domain: alpha-amylase core homology <AMY>
F:197/Binding site: carbonyl site (Asn) (covalent) #status experimental
F:210,230,297/Active site: His, Glu, Asp #status experimental

Query Match 93.3%; Score 2503.5; DB 2; Length 478;
Best Local Similarity 97.9%; Pred. No. 5.9e-172;
Matches 468; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY	21	ATPADWRSOSIYFLLTDRFARTDGSSTATCNTADQKYCGGTWQGIIDKLDYIOGMGFTAI	80
DB	1	ATPADWRSOSIYFLLTDRFARTDGSSTATCNTADQKYCGGTWQGIIDKLDYIOGMGFTAI	60
QY	81	WITPVTAQPLQTTAYGDVHYGQQDIYSLNENYGTADDLKALSSALHGRMYLMDVVDV	140
DB	61	WITPVTAQPLQTTAYGDVHYGQQDIYSLNENYGTADDLKALSSALHGRMYLMDVVDV	120
QY	141	NEMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQYEDQTOVEDCWLGDNVSLPDLDTTK	200
DB	121	NEMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQYEDQTOVEDCWLGDNVSLPDLDTTK	180
QY	201	DVVKNEWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC	260
DB	181	DVVKNEWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC	240
QY	261	PYQNVMDGVLYPIYPLNAPKSTSGSMDLLYNMINTVKSDCPDSTLLGTFVENHNDNPR	320
DB	241	PYQNVMDGVLYPIYPLNAPKSTSGSMDLLYNMINTVKSDCPDSTLLGTFVENHNDNPR	300
QY	321	FASYTNDIALAKNVAAFIILNDGIPYIYAGQHQHYAGNDPANREATWLSGYPTDSELYK	380
DB	301	FASYTNDIALAKNVAAFIILNDGIPYIYAGQHQHYAGNDPANREATWLSGYPTDSELYK	360
QY	381	LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTGDSQIYVILSNKGASGDSY	440
DB	361	LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTGDSQIYVILSNKGASGDSY	419
QY	441	LSLSGAGYTAGOOLTEVIGCTTVTVGSDGNVPPVPMAGGLPRVLYPTEKLAGSKICSSS	498
DB	420	LSLSGAGYTAGOOLTEVIGCTTVTVGSDGNVPPVPMAGGLPRVLYPTEKLAGSKICSDS	477

RESULT 9
A35282
alpha-amylase (EC 3.2.1.1) - Aspergillus niger
C:Species: Aspergillus niger
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A35282
R:Boel, E.; Brady, L.; Brzozowski, A.M.; Derewenda, Z.; Dodson, G.G.; Jensen, V.J.; Pet
Biochemistry 29, 6244-6249, 1990
A:Title: Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-angstrom
A:Reference number: A35282; PMID:91002514; PMID:2207069
A:Accession: A35282
A:Molecule type: mRNA
A:Residues: 1-484 <BOE>
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:173-300/Domain: alpha-amylase core homology <AMY>

Query Match 66.3%; Score 1780; DB 1; Length 484;
Best Local Similarity 67.2%; Pred. No. 5.1e-120;
Matches 319; Conservative 63; Mismatches 93; Indels 0; Gaps 0;

QY	24	ADWRSOSIYFLLTDRFARTDGSSTATCNTADQKYCGGTWQGIIDKLDYIOGMGFTAIWIT	83
DB	4	ADWRSOSIYFLLTDRFARTDGSSTATCNTADQKYCGGTWQGIIDKLDYIOGMGFTAIWIS	63
QY	84	PVTAQPLQTTAYGDVHYGQQDIYSLNENYGTADDLKALSSALHGRMYLMDVVDVANH	143
DB	64	PIEQPLQTTADGEAHVGYGQQDIYDVSNSNFTADDLSLSALHARGMYLMDVVDVANH	123
QY	144	GYDAGSSVDYSVFKPFSSQDYFHPFCFIQYEDQTOVEDCWLGDNVSLPDLDTTKDV	203
DB	124	GYAGNDVDYSVFPDFDSSSYFHPYCLITDNLTMVQDCWEGDITVSLPDLNLTETAV	183
QY	204	KNEWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC	263

Db 184 RTIWDVADLVSNVSDGLRIDSVLEVPDFPPQYQEAAGVYCVGEVDNGNPNALDCPYQ 243

Qy 264 NVMDGVLNYPPIYPLINAFKSTSGSMDLYNNMINTVKSPDSTLLGTVEHNDNPRFAS 323

Db 244 KVLGDVLNPTTWQLYAFESSGSLNLYNMKSVASDCSDPTLLGNFIENHNDNPRFAS 303

Qy 324 YTNDAIAKNVAAFIILNDGIPPIIYAGQHQYAGGNDPANREATWLSGYPTDSELYKLTJA 383

Db 304 YTSYSQAQNVLSYIFLSDGIPVIYAGEBQHYSGGKVPYNREATWLSGYDTSAELYTWIA 363

Qy 384 SANATRYAISKDTGHTVYKNWPIYKDDTTIAMRKGTGDSQIVITLSNKGASGDSYTLSL 443

Db 364 TTNAIRKLAISADSAITYANDAFYDTSNTIAMRKGTSGSIVITLSNKGSSGSSYTLTL 423

Qy 444 SGAGYTAGOOLTEVIGCTTVTGSGNVVPVPMAGGLPRVLYPTEKLAGSKICSSS 498

Db 424 SSGSYTGKLEIYATCTSVTVDDSGDIIPVMASGLPVLFPASVVDSSSLCGGS 478

RESULT 10

JC4510

pullulanase (EC 3.2.1.41) precursor - yeast (lipomyces kononenkoae)

N:Alternate names: LKAL protein; raw starch-degrading amylase

N:Contains: alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)

C:Species: Lipomyces kononenkoae

C:Date: 07-Feb-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004

C:Accession: JC4510; PC4116

R:Steyn, A.J.C.; Marmur, J.; Pretorius, I.S.

Gene 166, 65-71, 1995

A:Title: Cloning, sequence analysis and expression in yeasts of a cDNA containing a LipD

A:Reference number: JC4510; MUID:96105202; PMID:8529895

A:Accession: JC4510

A:Molecule type: mRNA

A:Residues: 1-624 <STB>

A:Cross-References: UNIPROT:Q01117; GB:U030376; NID:g1173536; PIDN:AAC49622.1; PID:g11735

A:Experimental source: strain IGC4052B

A:Accession: PC4116

A:Molecule type: protein

A:Residues: 29-44 <ST2>

A:Experimental source: IGC4052B

C:Genetics:

A:Gene: LKAL

C:Function:

A:Description: hydrolyzes raw starch, degrading both alpha-1,4 and alpha-1,6 linkages

A:Pathway: glycogen/starch degradation

C:Superfamily: Lipomyces alpha-amylase; alpha-amylase core homology; glucoamylase starch

C:Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide

F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-624/Product: alpha-amylase #status predicted <WAT>

F:48-141/Domain: glucoamylase starch-binding domain homology <SBD>

F:320-447/Domain: alpha-amylase core homology <AMY>

F:177-185,297-311,387-430,587-622/Disulfide bonds: #status predicted

F:304,344/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:357,377,444/Active site: His, Glu, Asp #status predicted

Query Match 60.7%; Score 1629; DB 1; Length 624;

Best Local Similarity 60.6%; Pred. No. 5e-109;

Matches 292; Conservative 77; Mismatches 113; Indels 0; Gaps 0;

Qy 15 AAPALAAPADWRSQSIFLLTDRPARTDGTSTATCNTADQKCGGTWQGIIDKLDYIQG 74

Db 142 SASVPTGTAAWNRGSIYQVVTDRPARTDGTSTYSCDVTDVYCGSVYRGIINMLDYIQG 201

Qy 75 MGFTAIWLTPTVAQLPQTAYGDAYHGYWQDIYSLNENYGTADDLKALSSALHERGMYL 134

Db 202 MGFTAIWLSPIVENIPDDTGYGAYHGYWMDIFALTNFPGADDLIALATELHNRGMYL 261

Qy 135 MYDVVANHMGYDAGSSVDYSVFKEPFSQDYFHPFCFIQNYEDQTVQVEDCWLGDNTVSLP 194

Db 262 MVDIVVNHFAGSGNHADVSEYFPYSSQDYFHSFCWITDYSNQTNVEECWLGDSSVPLV 321

Qy 195 LDLTTKDVVKNEWDVWGLSVSNYSIDGLRIDTVKHQKDFPFGYKNKAAGVYICEVLDG 254

Db 322 DVNTQLDVTKSEQSWAKQLIANYSIDGLRIDTVKHQVQDFWAPFQEAAGIYTVGEVFDG 381

Qy 255 DPAYTCPTQNVMDGVNLNPIYPIPLINAFKSTSGSMDLLYNNMINTVKSDCPDSDTLLGTTFVE 314

Db 382 DPSYTCPTQENLDGVNLNPPVYVVSFAQRVGSGISLSDVMDITLTKSECIDTTLTLLGSFLE 441

Qy 315 NHDNPRFASVYTNDAIAKNVAAFIILNDGIPPIIYAGQHQYAGGNDPANREATWLSGYPT 374

Db 442 NQDNPRFYSYTSDESILKNATAFTILSDGIPPIIYGOEQGLNGNDPYNREALWPTGYST 501

Qy 375 DSELYKLJASANAIRYAIKSDTGFVTYKNWPIYKDDTTIAMRKGTGDSQIVITLSNKG 434

Db 502 TSTFVEYIASLNQIRNHAIIYIDDTVLTQNVWVIYSDSTTIAMRKGTGFTGNQIITVLSNLGS 561

Qy 435 SCDSYTSLSGAGYTAGOOLTEVIGCTTVTGSGDNVVPVPMAGGLPRVLYPTEKLAGSKI 494

Db 562 SSGSYTLLSNTGXTASSVYVYBILTCTAVTVDLGNLAVPMSSGGLPRFYPESQLVGSGI 621

Qy 495 CS 496

Db 622 CS 623

RESULT 11

S33921

alpha-amylase (EC 3.2.1.1) SWA2 precursor - yeast (Schwanniomyces occidentalis)

N:Alternate names: alpha-1,4 glucanohydrolase

C:Species: Schwanniomyces occidentalis

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: S33921

R:Claros, M.G.; Abarca, D.; Fernandez-Lobato, M.; Jimenez, A.

Curr. Genet. 24, 75-83, 1993

A:Title: Molecular structure of the SWA2 gene encoding an AMY1-related alpha-amylase fro

A:Reference number: S33921; MUID:93365041; PMID:8358835

A:Accession: S33921

A:Molecule type: DNA

A:Residues: 1-507 <CLA>

A:Cross-References: UNIPROT:Q08806; EMBL:X73497; NID:g396561; PIDN:CAA51912.1; PID:g3965

C:Genetics:

A:Gene: SWA2

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-507/Product: alpha-amylase #status predicted <WAT>

F:205-332/Domain: alpha-amylase core homology <AMY>

F:134,229/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.9%; Score 1527; DB 2; Length 507;

Best Local Similarity 57.7%; Pred. No. 7.8e-102;

Matches 286; Conservative 74; Mismatches 130; Indels 6; Gaps 3;

Qy 1 MVAWMSFLYGLQVAAPALAAPADWRSQSIFLLTDRPARTDGTSTATCNTADQKCGG 60

Db 17 LVASKPIFLSKRDAGSSAAA---WRSESIYQLVTDRAFTDGTSTATCNTGDRVYCGG 72

Qy 61 TWQGIIDKLDYIQGFTAIWITPTVAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL 120

Db 73 TFOGIIDKLDYIQGFTAIWISPVVEQIPDGTGYAYHGYWMDKIYAINSNFQTADDL 132

Qy 121 KALSSALHERGMYLMDVVANHMGYDAGSSVDYSVFKEPFSQDYFHPFCFIQNYEDQTV 180

Db 133 KNLSELHKNRKNKLMVDIVTNHYAWNGAGSSVAISNYPNFQOQSYFHDYCLITNTDDQTN 192

Qy 181 VEDCWLGDNVTSLPDLDTTKDVVKNEWDVWGLSVSNYSIDGLRIDTVKHQKDFPFGYN 240

Db 193 VEDCWEGDNVTSLPDLRTEDSDVSSIENLWVAELVSNYSIDGLRIDSAKHVDESYPFSQ 252

Qy 241 KAAGVYICEVLDGDPATCTCPYQNVMDGVNLNPIYPIPLINAFKSTSGSMDLLYNNMINTVK 300

Db 253 SAAGVYLLGEVYDGDYPATCTCPYQNVMSGVNTYPLYPMLRFQFGTSNVDENAMISSLE 312

A:Reference number: S00064; MUID:87276512; PMID:3497057

A:Accession: S00064

A:Molecule type: DNA

A:Residues: 1-494 <ITO>

A:Cross-references: UNIPROT:P21567; EMBL:X05791; NID:G4847; PIDN:CAA29233.1; PID:G4848
A>Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in having 368-Thr

C:Genetics:

A:Gene: ALP1

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C:Keywords: calcium; extracellular protein; glycoprotein; glycosidase; hydrolase; metal

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-494/Product: alpha-amylase #status predicted <MAT>

F:200-327/Domain: alpha-amylase core homology <AMY>

F:57-65,177-191,267-310,462-493/Disulfide bonds: #status predicted

F:148,189,202,237/Binding site: calcium (Asn, Gln, Asp, His) #status predicted

F:224/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:233,257,324/Active site: Asp, Glu, Asp #status predicted

Query Match 52.1%; Score 1397.5; DB 1; Length 494;
Best Local Similarity 52.5%; Pred. No. 1.5e-92;
Matches 264; Conservative 83; Mismatches 129; Indels 27; Gaps 6;

QY 12 LQVAAPALAA-----TPAD-WRSQSIYFLLTDRFARTDGSSTTATCNTA 53

DB 1 MQISKAALLASIALVYAQPVTFLFRETNADKWRSQSIYQIVTDRFARTDGSSTASCNTE 60

QY 54 DKQYCGGTWQGIIDKLDYIQGMGFTAIWITPTAQLPQTAYGDYHGYWQODIYSLNEN 113

DB 61 DRLYCGSGFQGIIDKLDYIKDMGFTAIWISPVVENIPONTAYGYAHGYWKNVIYKINEN 120

QY 114 YGTADDLKALSALHERGMYLMDVVAHMGVDGAGSSVDYSVFPFSSQDYFHPFCFIQ 173

DB 121 FGTADDLKLSLAQELHDDRLMLMDVITVTHYSGDGSIDYSEYTPFNQDKYFHNICYLIS 180

QY 174 NYEDQTOVEDCWLGNTVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKHQK 233

DB 181 NYDDAQVQSCWEGDSSVALPDLRTEDSDVASVFNWKFVGNYSIDGLRIDSAKHVDQ 240

QY 234 DFWPGYNKAAGYCIGEVLGDGPAYTCYQNVMDGLNPIYPIYPLNNAFKSTSGSMDLY 293

DB 241 GFFPDFVASGVYSGVEYFGQDPAYTCPYQNVIPGVSNVPLYYPTTRFFKTTDSSSEL 300

QY 294 NMINTVKSQDCPDSTLLGTFVENHNDNPFASYNNDIALAKNVAAPFIILNDGPIIYAGQEQ 353

DB 301 QMISSVASSCSPTLLTNFVENHNDNPFASMTSDQSLSNAIAFAVLLGDPVPIYYGQEQ 360

QY 354 HYAGGNDPANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTT 413

DB 361 GLSGKSDPNREALWLSGYNKESDYKLIAKANAARNAAYQDSSYATSQLSVFSDHV 420

QY 414 IAMRKGTGDSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTVTVGSDGNVPV 473

DB 421 IATKRGS---VVSFNNLGGSSGS-DVTISNTGYSSGDELVEVLTCSTVSGSSD--LQV 473

QY 474 PWAGGLPRVLYPTEKLAGSKICS 496

DB 474 SIQGGQPIQIFVPAK--YASDICS 494

RESULT 15

S72270

alpha-amylase (EC 3.2.1.1) precursor - *Cryptococcus* sp. (strain CS2)

C:Species: *Cryptococcus* sp.

A:Variety: strain CS2

C:Date: 23-Apr-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

A:Accession: S72270

R:Refuji, H.; Chino, M.; Kato, M.; Iimura, Y.

Biochem. J. 318, 989-996, 1996

A:Title: Raw-starch-digesting and thermostable alpha-amylase from the yeast *Cryptococcus*

A:Reference number: S72270; MUID:96433120; PMID:8836148

A:Accession: S72270

A:Molecule type: DNA

A:Residues: 1-631 <IEF>

A:Cross-references: UNIPROT:Q92394; EMBL:D83540; NID:G1595852; PIDN:BAAL2010.1; PID:G159

A:Experimental source: strain S-2

C:Genetics:

A:Gene: amy-CS2

A:Introns: 289/2; 326/2

C:Function:

A:Pathway: glycogen/starch degradation

C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-631/Product: alpha-amylase #status predicted <MAT>

F:206-335/Domain: alpha-amylase core homology <AMY>

Query Match 47.1%; Score 1264; DB 2; Length 631;
Best Local Similarity 49.2%; Pred. No. 8e-83;
Matches 251; Conservative 84; Mismatches 153; Indels 22; Gaps 9;

QY 9 LYGLQVAAPALAA--TPADWRSQSIYFLLTDRFARTDGSSTTATCNTAQ--KYCGGTWQG 64

DB 7 LAGALLASLGLVAGLSPAEWSQSIYQVVTDRFALDNGNSPSCSGQSELNLYCNGTTFAG 66

QY 65 IIDKLDYIQGMGFTAIWITPTAQLP-----QTTAYGDYHGYWQODIYSLNENYGTADD 119

DB 67 IIDKLDYIQNMGTAIWISPVVKNIIDGSPNGYTPDGSAYHGYWAQDIYEINPHFGGASG 126

QY 120 LKALSSALHERGMYLMDVVAHMGY-----DGAGSSVDYSVFKPFSSQDYFHPFCFI 172

DB 127 LTDLISNALSRLGMYLMDVVAHMGYCGTDGCGPGNSVNYGSPFPENSEYFHPFCBI 186

QY 173 QNYEDQTOVEDCWLGNTVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQ 232

DB 187 -DYNRTSILDCWEGDEIVPLVDLRTEDSDVQSIFNSWISNLIQTYNIDGLRIDSLQOQSG 245

QY 233 KDFWPGYNKAA-GVYCIGEVLGDGPAYTCPYQNV-MDGLNPIYPIYPLNNAFKSTSGSMD 290

DB 246 SFFPFGFNAAGMYWGEVFNQSPYVCPYQAGMPGLNYPMEFYITNAFQTSSSGMS 305

QY 291 DLYNMINTVKSQDCPDSTLLGTFVENHNDNPFASYNNDIALAKNVAAPFIILNDGPIIYAG 350

DB 306 QLAQGISAMQSDCSDTTLGSLFLENQDNPRFPSTSLDTRAQNAIAFTMLQDGIPIYYG 365

QY 351 QEOHVAGGNDPANREATWLS-GYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYK 409

DB 366 QEOHLSGSGVPLNREALWTSGGYDTSSPLYEMITTVNQLRTLAIKQNGGFVYKIQVPYT 425

QY 410 DDTTIAMRKGTGDSQIVTILSNKGASGDSYTLISLGA--GYTAGQQLTEVIGCTTVTVGS 467

DB 426 DSNHIVTRKNSGYQIVGVYTVNGSAGSSSTLISSETGTGFSQASEPVMVLSCTLYHTGT 485

QY 468 DGNVPVPMAGGLPRVLYPTEKLAGSKICS 497

DB 486 DGSLSFTMTGGLPRVFNATLABSSLCCT 515

Search completed: November 7, 2005, 18:58:45

Job time : 59.6834 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:24:00 ; Search time 267.266 Seconds
(without alignments)
954.162 Million cell updates/sec

Title: US-10-820-200-2
Perfect score: 2684
Sequence: 1 MWAWNSFLYGLQVAAPALA.....LPRVLPTFKLAGSKICSSS 498

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 01: *
1: uniprot_prot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	ID	Description
1	2684	100.0	498	2 Q76CT3	Q76ct3 aspergillus
2	2684	100.0	499	1 AMYA_ASPOR	P10529 aspergillus
3	2680	99.9	499	2 Q76L99	Q76l99 aspergillus
4	2675	99.7	499	1 AMY_ASPSH	P30292 aspergillus
5	2674	99.6	499	1 AMYB_ASPAW	Q02906 aspergillus
6	2674	99.6	499	2 Q96TH4	Q96th4 aspergillus
7	2674	99.6	499	2 Q7LV45	Q7lv45 aspergillus
8	2662	99.2	498	1 AMYA_ASPAW	Q02905 aspergillus
9	1826	68.0	490	2 Q9UV07	Q9uv07 emericella
10	1810	67.4	640	2 Q13296	O13296 aspergillus
11	1791	66.7	634	2 Q76L96	Q76l96 aspergillus
12	1778	66.2	484	1 AMYA_ASPNG	P56271 aspergillus
13	1725.5	64.3	623	2 Q9UV09	Q9uv09 emericella
14	1662	61.9	647	2 Q6YF33	Q6yf33 lipomyces s
15	1629	60.7	624	1 AMY1_LIPKO	Q01117 lipomyces k
16	1527	56.9	507	1 AMY2_DBOC	Q08806 debaryomyce
17	1449	54.0	512	1 AMY1_DBOC	P19269 debaryomyce
18	1397.5	52.1	494	1 AMY1_SACFI	P21567 saccharomyc
19	1272.5	47.4	492	2 Q7SDJ6	Q7sdj6 neurospora
20	1264	47.1	631	2 Q92394	Q92394 cryptococcu
21	1056.5	39.4	533	2 Q7S4K0	Q7s4k0 neurospora
22	1015.5	37.8	513	1 AMY3_SCHPO	O14154 schizosacch
23	963.5	35.9	625	2 Q74922	Q74922 schizosacch
24	920.5	34.3	491	2 O13996	O13996 schizosacch
25	899	33.5	581	1 AMY1_SCHPO	Q09840 schizosacch
26	898.5	33.5	564	1 AMY4_SCHPO	Q9y789 schizosacch
27	898	33.5	478	1 YQZ9 SCHPO	Q10427 schizosacch
28	895	33.3	499	2 Q8J1E4	Q8j1e4 lipomyces k
29	737	27.5	482	2 Q60051	Q60051 thermoactin
30	670	25.0	1196	1 AMYB_PAEPO	P21543 paenibacill
31	653.5	24.3	774	1 AMY2_SCHPO	O42318 schizosacch

32	481.5	17.9	642	2 Q8Z0C9	Q8z0c9 anabaena sp
33	479.5	17.9	642	2 Q8RMG0	Q8rmg0 nostoc sp.
34	461.5	17.2	877	2 Q87FT5	Q87ft5 vibrio para
35	456.5	17.0	713	1 CDGT_BACSO	P05618 bacillus sp
36	454.5	16.9	712	1 CDGT_BACS3	P09121 bacillus sp
37	453	16.9	1798	2 Q9KZ11	Q9kz11 streptomyce
38	450	16.8	719	1 AMYM_BACST	P19531 bacillus st
39	447.5	16.7	712	2 Q6S3E3	Q6s3e3 bacillus sp
40	447.5	16.7	713	2 Q9F5W3	Q9f5w3 bacillus ci
41	444.5	16.6	713	2 CDGT_BAC11	P30921 bacillus sp
42	440.5	16.4	528	1 AMY_BACCI	P08137 bacillus ci
43	436	16.2	1806	2 Q82AS4	Q82as4 streptomyce
44	433	16.1	710	1 CDGT_THETU	P26827 thermoanaer
45	430.5	16.0	524	2 Q8R900	Q8r900 thermoanaer

ALIGNMENTS

RESULT 1

ID	Q76CT3	PRELIMINARY;	PRT;	498 AA.
AC	Q76CT3;			
DT	05-JUL-2004 (Tremblrel. 27, Created)			
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	Alpha-amylase.			
GN	Name=amyA;			
OS	Aspergillus kawachi (Aspergillus awamori var. kawachi).			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;			
OC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.			
OX	NCBI_TaxID=40384;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Ito K.;			
RL	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.			
CC	-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.			
DR	EMBL; AB109452; BAD01051.1; ..			
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.			
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro; IPR006047; Alpha amyl cat.			
DR	InterPro; IPR006589; Alp amyl cat sub.			
DR	InterPro; IPR006046; Glyco_hydro_13.			
DR	Fram; PF00128; Alpha-amylase; 1.			
DR	PRINTS; PRO0110; ALPHAAMYLASE.			
DR	SMART; SM00642; Amy; 1.			
SQ	SEQUENCE 498 AA; 54679 MW; 8407BBFC7F4E3FC0 CRC64;			

Query Match	100.0%;	Score 2684;	DB 2;	Length 498;
Best Local Similarity	100.0%;	Fred. No. 2e-178;		
Matches 498;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 MWAWNSFLYGLQVAAPALAATPADWRSQSIYFLLTDRPARTDGTATCNTADQKCGG	60		
DB	1 MWAWNSFLYGLQVAAPALAATPADWRSQSIYFLLTDRPARTDGTATCNTADQKCGG	60		
QY	61 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDAYHGYWQQDIYSLNENYGTADDL	120		
DB	61 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDAYHGYWQQDIYSLNENYGTADDL	120		
QY	121 KALSSALHGRMYLVVDVNVANHWGVDGAGSSVDYSVFKPFPSSQDYHPHPCFQNYEDQIQ	180		
DB	121 KALSSALHGRMYLVVDVNVANHWGVDGAGSSVDYSVFKPFPSSQDYHPHPCFQNYEDQIQ	180		
QY	181 VEDCWLGNMTVSLPDLDTTKDVVKNWYDWVSLVSNYSIDGLRIDTVKHVKQDFWPGYN	240		
DB	181 VEDCWLGNMTVSLPDLDTTKDVVKNWYDWVSLVSNYSIDGLRIDTVKHVKQDFWPGYN	240		
QY	241 KAAGVYICIGVLDPGDPAYTCPYQNVMDGVNLNPIYYPYLLNAPKSTSGSMDLLNMTNVT	300		
DB	241 KAAGVYICIGVLDPGDPAYTCPYQNVMDGVNLNPIYYPYLLNAPKSTSGSMDLLNMTNVT	300		
QY	301 SDCPSTLLGTFFVHNDRPFASNTYNDIALAKNVAAFIINDGIPPIYAGQEQHYAGGND	360		

Db 301 SDPCDSTLLGTFVFNHNDNPRFASNTNDIALKNVAAFIILNDGIPITVAGQOHVAGND 360
Qy 361 PANRATWLSGVPDSELYKLTASANAIRNVAISKDTGVTYKNWPIYKDDTTIARKGT 420
Db 361 PANRATWLSGVPDSELYKLTASANAIRNVAISKDTGVTYKNWPIYKDDTTIARKGT 420
Qy 421 DGSQIVTILSNKGASDSTYLSLSGAGYTAGQOLTEVIGCTTIVGSDGNVFPVWAGGLP 480
Db 421 DGSQIVTILSNKGASDSTYLSLSGAGYTAGQOLTEVIGCTTIVGSDGNVFPVWAGGLP 480
Qy 481 RVLYPTEKLAGSKICSSS 498
Db 481 RVLYPTEKLAGSKICSSS 498

RESULT 2
AMTA ASPOR
ID AMYA ASPOR STANDARD; PRT; 499 AA.
AC P10529; P11763; Q00250;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-D-glucanase precursor (EC 3.2.1.1) (Taka-amylase A) (TAA) (1,4-
GN Name=AMY1;
GN and
GN Name=AMY2;
GN and
GN Name=AMY3;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 63303;
RX MEDLINE=89237897; PubMed=2785629;
RA Wiesel S., Lachmund A., Wildhardt G., Rutkowski E.;
RT "Three alpha-amylase genes of Aspergillus oryzae exhibit identical
RT intron-exon organization.";
RL Mol. Microbiol. 3:3-14(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6;
RA Genes M.J., Dove M.J., Seligy V.L.;
RT "Aspergillus oryzae has two nearly identical Taka-amylase genes, each
RT containing eight introns.";
RL Gene 79:107-117(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
RA Tsukagoshi N., Furukawa M., Nagaba H., Kirita N., Tsuboi A., Uda S.;
RT "Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A:
RT evidence for multiple related genes.";
RL Gene 84:319-327(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
RA Tsukagoshi N., Furukawa M., Nagaba H., Kirita N., Tsuboi A., Uda S.;
RT "Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A:
RT evidence for multiple related genes.";
RL Gene 84:319-327(1989).
RN [5]
RP SEQUENCE OF 22-499.
RA Toda H., Kondo K., Narita K.;
RT "The complete amino acid sequence of Taka-amylase A.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 58:208-212(1982).
RN [6]
RP SEQUENCE OF 206-225.
RX MEDLINE=74001521; PubMed=4733850;
RA Isemura S., Ikenaka T.;
RT "The amino acid sequences of glycopeptides obtained from Taka-amylase
RT A with trypsin and chymotrypsin.";

J. Biochem. 74:1-10(1973).
RN [7]
RP SEQUENCE OF 433-499.
RA Narita K.;
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=80227691; PubMed=6156152;
RA Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
RT Toda H., Narita K., Kakudo M.;
RT "Molecular structure of taka-amylase A. I. Backbone chain folding at
RT 3-A resolution.";
RL J. Biochem. 87:1555-1558(1980).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=84212370; PubMed=6609921;
RA Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
RT "Structure and possible catalytic residues of Taka-amylase A.";
RL J. Biochem. 95:697-702(1984).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
RX MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
RA Brzozowski A.M., Davies G.J.;
RT "Structure of the Aspergillus oryzae alpha-amylase complexed with the
RT inhibitor acarbose at 2.0-A resolution.";
RL Biochemistry 36:10837-10845(1997).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations.
CC -!- SUBUNIT: Monomer.
CC -!- BIOTECHNOLOGY: Used in the brewing industry to increase the
CC fermentability of beer worts (including those made from unmalted
CC cereals), in the starch industry to make high maltose and high DE
CC syrups (starch saccharification), in the alcohol industry to
CC reduce fermentation time, in the cereal food industry for flour
CC supplementation and improvement of chilled and frozen dough, and
CC in the forestry industry for low-temperature modification of
CC starch. Sold under the name Fungamyl by Novozymes.
CC -!- MISCELLANEOUS: The sequence of AMY1 and AMY2 is shown.
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X12725; CAA31218.1; -;
DR EMBL; X12726; CAA31219.1; -;
DR EMBL; X12727; CAA31220.1; -;
DR EMBL; D00434; BAA00336.1; -;
DR EMBL; M33218; AAA32708.1; -;
DR PIR; JK0201; JK0201.
DR PIR; JT0456; JT0466.
DR PIR; S04548; ALAS1.
DR PDB; 2TAA; X-ray; A=22-499.
DR PDB; 6TAA; X-ray; @=22-499.
DR PDB; 7TAA; X-ray; @=22-499.
DR GlycoSuiteDB; P10529; -;
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Aamy; 1.
DR 3D-structure; Calcium-binding; Carbohydrate metabolism;
KW Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
KW Multigene family; Signal.
FT SIGNAL 1 21
FT CHAIN 22 499 Alpha-amylase A.

Query Match 99.9%; Score 2680; DB 2; Length 499;
 Best Local Similarity 99.8%; Pred. No. 3.9e-178;
 Matches 497; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAATPADWRSOSIYFLLTDRPARTDGGTTATCNTADQKCGG 60
 DB 2 MVAMWSFLYGLQVAAPALAAATPADWRSOSIYFLLTDRPARTDGGTTATCNTADQKCGG 61
 QY 61 TWQGIIDKLDYIQGSGFTAIWITPTAQLPQTAYGDVHYGWQDIYSLNENYGTADDL 120
 DB 62 TWQGIIDKLDYIQGSGFTAIWITPTAQLPQTAYGDVHYGWQDIYSLNENYGTADDL 121
 QY 121 KALSSALHERGMYLMDVVANHMVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 180
 DB 122 KALSSALHERGMYLMDVVANHMVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 181
 QY 241 KAAGVYICGEVLDDGPAYTCYQNVMDGVLNPIYYPILLNAPKSTSGSMDDLNNINTVK 300
 DB 242 KAAGVYICGEVLDDGPAYTCYQNVMDGVLNPIYYPILLNAPKSTSGSMDDLNNINTVK 301
 QY 301 SDCPDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPIIYAGQBOHYAGGND 360
 DB 302 SDCPDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPIIYAGQBOHYAGGND 361
 QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKKNWPIYKDDTTIAMRGT 420
 DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKKNWPIYKDDTTIAMRGT 421
 QY 421 DGSQIVTILSNKAGSDSYTILSLGAGYTAGQQLTEVIGCTTTVVGSDGNVPPVPMAGGLP 480
 DB 422 DGSQIVTILSNKAGSDSYTILSLGAGYTAGQQLTEVIGCTTTVVGSDGNVPPVPMAGGLP 481
 QY 481 RVLVPTKLAGSKICSSS 498
 DB 482 RVLVPTKLAGSKICSSS 499

RESULT 4
 ID AMY ASPSH STANDARD; PRT; 499 AA.
 AC P30292;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase).
 GN Name=AMY;
 OS Aspergillus shirousami.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5070;
 RN [1]_
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92323146; PubMed=1368777;
 RA Shibuya I., Tamura G., Ishikawa T., Hara S.;
 RT "Cloning of the alpha-amylase cDNA of Aspergillus shirousami and its
 RT expression in Saccharomyces cerevisiae."
 RL Bionci. Biotechnol. Biochem. 56:174-179(1992).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations (By similarity).
 CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC -----
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DR EMBL; DI0461; BAA01255.1; -;
 DR HSSP; P10529; 7TAA.
 DR InterPro; IPR006589; Alp_aml cat sub.
 DR InterPro; IPR006047; Alpha_aml cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amyrase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Aamy; 1.
 KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 KW Hydrolase; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 499
 FT ACT_SITE 227 227 Alpha-amyrase.
 FT ACT_SITE 251 251 Nucleophile (By similarity).
 FT ACT_SITE 318 318 Proton donor (By similarity).
 FT METAL 142 142 By similarity.
 FT METAL 183 183 Calcium 1 (By similarity).
 FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 196 196 Calcium 1 (By similarity).
 FT METAL 227 227 Calcium 2 (By similarity).
 FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 251 251 Calcium 2 (By similarity).
 FT DISULFID 51 59 By similarity.
 FT DISULFID 171 185 By similarity.
 FT DISULFID 261 304 By similarity.
 FT DISULFID 461 496 By similarity.
 FT CARBOHYD 218 218 N-linked (GlcNAc...) (By similarity).
 SQ SEQUENCE 499 AA; 54852 MW; 1FB7AE50DA01C03F CRC64;

Query Match 99.7%; Score 2675; DB 1; Length 499;
 Best Local Similarity 99.8%; Pred. No. 8.6e-178;
 Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAATPADWRSOSIYFLLTDRPARTDGGTTATCNTADQKCGG 60
 DB 2 MVAMWSFLYGLQVAAPALAAATPADWRSOSIYFLLTDRPARTDGGTTATCNTADQKCGG 61
 QY 61 TWQGIIDKLDYIQGSGFTAIWITPTAQLPQTAYGDVHYGWQDIYSLNENYGTADDL 120
 DB 62 TWQGIIDKLDYIQGSGFTAIWITPTAQLPQTAYGDVHYGWQDIYSLNENYGTADDL 121
 QY 121 KALSSALHERGMYLMDVVANHMVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 180
 DB 122 KALSSALHERGMYLMDVVANHMVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 181
 QY 181 VEDCWLGDNTVSLPDLDTTKDVKNNEWDMVWGLSVSNYSIDGLRIDTVKHVKQDFWPGYN 240
 DB 182 VEDCWLGDNTVSLPDLDTTKDVKNNEWDMVWGLSVSNYSIDGLRIDTVKHVKQDFWPGYN 241
 QY 241 KAAGVYICGEVLDDGPAYTCYQNVMDGVLNPIYYPILLNAPKSTSGSMDDLNNINTVK 300
 DB 242 KAAGVYICGEVLDDGPAYTCYQNVMDGVLNPIYYPILLNAPKSTSGSMDDLNNINTVK 301
 QY 301 SDCPDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPIIYAGQBOHYAGGND 360
 DB 302 SDCPDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPIIYAGQBOHYAGGND 361
 QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKKNWPIYKDDTTIAMRGT 420
 DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKKNWPIYKDDTTIAMRGT 421
 QY 421 DGSQIVTILSNKAGSDSYTILSLGAGYTAGQQLTEVIGCTTTVVGSDGNVPPVPMAGGLP 480
 DB 422 DGSQIVTILSNKAGSDSYTILSLGAGYTAGQQLTEVIGCTTTVVGSDGNVPPVPMAGGLP 481
 QY 481 RVLVPTKLAGSKICSSS 498
 DB 482 RVLVPTKLAGSKICSSS 499

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RESULT 5
AMYB ASPAW STANDARD; PRT; 499 AA.
ID AMYB ASPAW
AC Q02906;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase B).
GN Name:AMYB;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DVUK143F;
RX MEDLINE=90254827; PubMed=2340501;
RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
RA Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
RT "Cloning, characterization, and expression of two alpha-amylase genes
RT from Aspergillus niger var. awamori.";
RL Curr. Genet. 17:203-212 (1990).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X52756; CAA36967.1; -.
DR PIR; B48305; B48305.
DR HSP; P10529; 7TAA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
KW Hydrolase; Multigene family; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 499 Alpha-amylase B.
FT ACT_SITE 227 227 Nucleophile (By similarity).
FT ACT_SITE 251 251 Proton donor (By similarity).
FT ACT_SITE 318 318 By similarity.
FT METAL 142 142 Calcium 1 (By similarity).
FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
FT similarity).
FT METAL 196 196 Calcium 1 (By similarity).
FT METAL 227 227 Calcium 2 (By similarity).
FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
FT similarity).
FT METAL 251 251 Calcium 2 (By similarity).
FT DISULFID 51 59 By similarity.
FT DISULFID 171 185 By similarity.
FT DISULFID 261 304 By similarity.
FT DISULFID 461 496 By similarity.
FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 499 AA; 54921 MW; 740B96B11BC01A8A CRC64;
Query Match 99.6%; Score 2674; DB 1; Length 499;
Best Local Similarity 99.6%; Pred. No. 1e-177; 2; Indels 0; Gaps 0;
Matches 496; Conservative 0; Mismatches 2;

```

RESULT 6

Q96TH4

ID Q96TH4 PRELIMINARY; PRT; 499 AA.

AC Q96TH4;

DT 01-DEC-2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE Taka-amylase A (EC 3.2.1.1).

GN Name=amyA;

OS Aspergillus oryzae.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

OX NCBI_TaxID=5062;

RN [1] SEQUENCE FROM N.A.

RP STRAIN=RI840.

RX MEDLINE=20289310; PubMed=10830498;

RA Gomi K., Akeno T., Minecoki T., Ozeki K., Kumagai C., Okazaki N.,

RA Iimura Y.;

RT "Molecular cloning and characterization of a transcriptional activator

RT gene, amyR, involved in the amyolytic gene expression in Aspergillus

RT oryzae.";

RL Biosci. Biotechnol. Biochem. 64:816-827(2000).

CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

DR EMBL; AB021876; BAA95703.1; -.

DR PIR; JN0588; JN0588.

DR PIR; S04549; ALA83.

DR HSP; P10529; 7TAA.

DR GO; GO:0004556; F:alpha-amylase activity; IEA.

DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR006047; Alpha_amy1_cat.

DR InterPro; IPR006589; Alp_amy1_cat_sub.

DR InterPro; IPR006046; Glyco_hydro_13.

DR Pfam; PF00128; Alpha-amylase; 1.

DR PRINTS; PR00110; ALPHAAMYLASE.

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DR SMART; SM00642; Aamy; 1.  
KW Glycosidase; Hydrolase.  
SQ SEQUENCE 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;  
  
Query Match 99.6%; Score 2674; DB 2; Length 499;  
Best Local Similarity 99.6%; Pred. No. 1e-177;  
Matches 496; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MVAWNSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGSSTATCNTADOKYCGG 60  
DB 2 MVAWNSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGSSTATCNTADOKYCGG 61  
  
QY 61 TWQGIIDKLDYIQMGFTAIWTPVTAQLPQTAYGDAYHGYWQODIYSLNENYGTADDL 120  
DB 62 TWQGIIDKLDYIQMGFTAIWTPVTAQLPQTAYGDAYHGYWQODIYSLNENYGTADDL 121  
  
QY 121 KALSSALHERGMVLMVDVVAHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIONYEDQTO 180  
DB 122 KALSSALHERGMVLMVDVVAHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIONYEDQTO 181  
  
QY 181 VEDCWLGNTVSLPDLDTTKOVVKNEDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 240  
DB 182 VEDCWLGNTVSLPDLDTTKOVVKNEDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 241  
  
QY 241 KAAGYVCIGEVLGDGPAYTCPYQNVMDGVNLNPIYYPILLNAFKSTSGSMDDLNNMINTVK 300  
DB 242 KAAGYVCIGEVLGDGPAYTCPYQNVMDGVNLNPIYYPILLNAFKSTSGSMDDLNNMINTVK 301  
  
QY 301 SDCPDSTLLGTFFVENHNDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGND 360  
DB 302 SDCPDSTLLGTFFVENHNDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGND 361  
  
QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVTKNWPYKDDTTIAMRKT 420  
DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVTKNWPYKDDTTIAMRKT 421  
  
QY 421 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTTVTVGSDGNVPPVPMAGGLP 480  
DB 422 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTTVTVGSDGNVPPVPMAGGLP 481  
  
QY 481 RVLYPEKLAGSKICSSS 498  
DB 482 RVLYPEKLAGSKICSSS 499  
  
RESULT 7  
Q7LV45 PRELIMINARY; PRT; 499 AA.  
ID Q7LV45  
AC Q7LV45;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Alpha-amylose (EC 3.2.1.1).  
GN Name=amy1;  
OS Aspergillus flavus.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
OX NCBI_TaxID=5059;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=86-10D;  
RA Fakhoury A.M., Weloshuk C.P.;  
RT "Amy1, the alpha-amylose gene of Aspergillus flavus: Involvement in  
RT aflatoxin biosynthesis in maize kernels.";  
RL Phytopathology 89:908-914 (1999).  
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.  
DR EMBL; AF139925; AAF14264.1; -.  
DR GO; GO:0004556; F:alpha-amylose activity; IEA.  
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR006047; Alpha_amy1_cat.  
DR InterPro; IPR006589; Alp_amy1_cat_sub.  
DR InterPro; IPR006046; Alp_hydro_13.
```

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DR Pfam; PF00128; Alpha-amylose; 1.  
DR PRINTS; PR00110; ALPHAAMYLOSE.  
DR SMART; SM00642; Aamy; 1.  
KW Glycosidase; Hydrolase.  
SQ SEQUENCE 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;  
  
Query Match 99.6%; Score 2674; DB 2; Length 499;  
Best Local Similarity 99.6%; Pred. No. 1e-177;  
Matches 496; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MVAWNSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGSSTATCNTADOKYCGG 60  
DB 2 MVAWNSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGSSTATCNTADOKYCGG 61  
  
QY 61 TWQGIIDKLDYIQMGFTAIWTPVTAQLPQTAYGDAYHGYWQODIYSLNENYGTADDL 120  
DB 62 TWQGIIDKLDYIQMGFTAIWTPVTAQLPQTAYGDAYHGYWQODIYSLNENYGTADDL 121  
  
QY 121 KALSSALHERGMVLMVDVVAHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIONYEDQTO 180  
DB 122 KALSSALHERGMVLMVDVVAHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIONYEDQTO 181  
  
QY 181 VEDCWLGNTVSLPDLDTTKOVVKNEDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 240  
DB 182 VEDCWLGNTVSLPDLDTTKOVVKNEDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 241  
  
QY 241 KAAGYVCIGEVLGDGPAYTCPYQNVMDGVNLNPIYYPILLNAFKSTSGSMDDLNNMINTVK 300  
DB 242 KAAGYVCIGEVLGDGPAYTCPYQNVMDGVNLNPIYYPILLNAFKSTSGSMDDLNNMINTVK 301  
  
QY 301 SDCPDSTLLGTFFVENHNDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGND 360  
DB 302 SDCPDSTLLGTFFVENHNDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGND 361  
  
QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVTKNWPYKDDTTIAMRKT 420  
DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVTKNWPYKDDTTIAMRKT 421  
  
QY 421 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTTVTVGSDGNVPPVPMAGGLP 480  
DB 422 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTTVTVGSDGNVPPVPMAGGLP 481  
  
QY 481 RVLYPEKLAGSKICSSS 498  
DB 482 RVLYPEKLAGSKICSSS 499  
  
RESULT 8  
AMYA ASPAW STANDARD; PRT; 498 AA.  
ID AMYA ASPAW  
AC Q02905;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Alpha-amylose A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan  
DE glucanohydrolase A).  
GN Name=AMYA;  
OS Aspergillus awamori.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiales; Trichocomaceae; mitosporic trichocomaceae; Aspergillus.  
OX NCBI_TaxID=105351;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UVK143F;  
RX MEDLINE=90254827; PubMed=2340591;  
RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,  
RT Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;  
RT "Cloning, characterization, and expression of two alpha-amylose genes  
RT from Aspergillus niger var. awamori.";  
RL Curr. Genet. 17:203-212 (1990).  
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic  
CC linkages in oligosaccharides and polysaccharides.  
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
```


CC at high concentrations (By similarity).
 CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC -----
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 CC -----
 CC EMBL; X52755; CAA36966.1; -;
 CC PIR; A48305; A48305.
 CC HSP; P10529; 7TAA.
 CC InterPro; IPR006589; Alp_amy1_cat_sub.
 CC InterPro; IPR006047; Alpha_amy1_cat.
 CC InterPro; IPR006046; Glyco_hydro_13.
 CC Pfam; PF00128; Alpha-amy1ase; 1.
 CC PRINTS; PR00110; ALPHAAMYLASE.
 CC SMART; SM00642; Amy; 1.
 CC Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 KW Hydrolase; Multigene family; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 498 Alpha-amy1ase A.
 FT ACT_SITE 227 227 Nucleophile (By similarity).
 FT ACT_SITE 251 251 Proton donor (By similarity).
 FT ACT_SITE 318 318 By similarity.
 FT METAL 142 142 Calcium 1 (By similarity).
 FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 196 196 Calcium 1 (By similarity).
 FT METAL 227 227 Calcium 2 (By similarity).
 FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 251 251 Calcium 2 (By similarity).
 FT DISULFID 51 59 By similarity.
 FT DISULFID 171 185 By similarity.
 FT DISULFID 261 304 By similarity.
 FT DISULFID 461 496 By similarity.
 FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 498 AA; 54880 MW; 7658511BC01A8A01 CRC64;

Query Match 99.2%; Score 2662; DB 1; Length 498;
 Best Local Similarity 99.6%; Pred. No. 6.9e-177;

Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MWANSLFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGG 60
 DB 2 MWANSLFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGG 61
 QY 61 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHYGWQDDIYSLNENYGTADDL 120
 DB 62 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHYGWQDDIYSLNENYGTADDL 121
 QY 121 KALSSALHGERMYLVVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 180
 DB 122 KALSSALHGERMYLVVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 181
 QY 181 VEDCWLGDNTVSLPDLDTTKDVVKNEWDVWGLSVNSYISDGLRIDTVKHVKQDFWPGYN 240
 DB 182 VEDCWLGDNTVSLPDLDTTKDVVKNEWDVWGLSVNSYISDGLRIDTVKHVKQDFWPGYN 241
 QY 241 KAAGVYICIGVLDDGDPAYTCYQNVMDGVLYPIYPLLNAPFKSTSGSMDLLYNNINTVK 300
 DB 242 KAAGVYICIGVLDDGDPAYTCYQNVMDGVLYPIYPLLNAPFKSTSGSMDLLYNNINTVK 301
 QY 301 SDCPDSTLLGTFFVENHNDNPRFASYTNDIALAKNVAAPFIILNDGIPPIYAGQSHYAGGND 360
 DB 302 SDCPDSTLLGTFFVENHNDNPRFASYTNDIALAKNVAAPFIILNDGIPPIYAGQSHYAGGND 361
 QY 361 PANREATWLSGYPDSELYKLIASANAIRNYAISKDTGFVYKNWPIYKDDTTIAMRKGT 420
 DB 362 PANREATWLSGYPDSELYKLIASANAIRNYAISKDTGFVYKNWPIYKDDTTIAMRKGT 421

QY 421 DGSQIVTILSNKAGSDSYTILSGAGYTAGOOLTEVIGCTTTVVGSDGNVPVPMAGGLP 480
 DB 422 DGSQIVTILSNKAGSDSYTILSGAGYTAGOOLTEVIGCTTTVVGSDGNVPVPMAGGLP 481
 QY 481 RVLYPTEKLAGSKIC 495
 DB 482 RVLYPTEKLAGSKIC 496
 RESULT 9
 Q9UV07 PRELIMINARY; PRT; 490 AA.
 AC Q9UV07;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Alpha-amy1ase AmyA.
 GN Name=amyA;
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=162425;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Boase N.A., Murphy R.M., Kelly J.M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC EMBL; AF208225; AAF17103.1; -;
 DR HSP; P10529; 7TAA.
 DR GO; GO:0004556; F:alpha-amy1ase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amy1ase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 SQ SEQUENCE 490 AA; 54249 MW; A891C4ACEABE5305 CRC64;

Query Match 68.0%; Score 1826; DB 2; Length 490;
 Best Local Similarity 69.6%; Pred. No. 1e-118;

Matches 337; Conservative 53; Mismatches 92; Indels 2; Gaps 2;

QY 12 LQVAPALAAPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGGTWQGIIDKLDY 71
 DB 7 LQVAPALAAPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGGTWQGIIDKLDY 65
 QY 72 IQGMGFTAIWTPVTAQLPQTAYGDVHYGWQDDIYSLNENYGTADDL KALSSALHSG 131
 DB 66 IQGMGFTAIWTPVTAQLPQTAYGDVHYGWQDDIYSLNENYGTADDL KALSSALHSG 124
 QY 132 MYLVMDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTOVEDCWLGDNTV 191
 DB 125 MYLVMDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTOVEDCWLGDNTV 184
 QY 192 SLDPDLDTKDVVKNEWDVWGLSVNSYISDGLRIDTVKHVKQDFWPGYNKAAGVYICIGV 251
 DB 185 SLDPDLDTKDVVKNEWDVWGLSVNSYISDGLRIDTVKHVKQDFWPGYNKAAGVYICIGV 244
 QY 252 LQGDGPAYTCYQNVMDGVLYPIYPLLNAPFKSTSGSMDLLYNNINTVKSDCPDSTLLGT 311
 DB 245 LQGDGPAYTCYQNVMDGVLYPIYPLLNAPFKSTSGSMDLLYNNINTVKSDCPDSTLLGT 304
 QY 312 FVENHNDNPRFASYTNDIALAKNVAAPFIILNDGIPPIYAGQSHYAGGNDPANREATWLSG 371
 DB 305 FVENHNDNPRFASYTNDIALAKNVAAPFIILNDGIPPIYAGQSHYAGGNDPANREATWLSG 364
 QY 372 YPTDSELYKLIASANAIRNYAISKDTGFVYKNWPIYKDDTTIAMRKGTGDSQIVTILSN 431
 DB 365 YPTDSELYKLIASANAIRNYAISKDTGFVYKNWPIYKDDTTIAMRKGTGDSQIVTILSN 424
 QY 432 KASGSDSYTILSNKAGSDSYTILSGAGYTAGOOLTEVIGCTTTVVGSDGNVPVPMAGGLP 491

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Db 425 AGADAGSSVSPVNTGFTAGAAVTEIYTCEDITVSGSGEVSPMESGLPRVLYPKALEG 484
QY 492 SKIC 495
Db 485 SGIC 488

RESULT 10
O13296
ID O13296 PRELIMINARY; PRT; 640 AA.
AC O13296;
DT 01-JAN-1998 (TREMELrel. 05, Created)
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Acid-stable alpha-amylose.
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaneko A., Sudo S., Sakamoto Y., Tamura G., Ishikawa T., Ohba T.;
RT "Molecular-cloning and determination of the nucleotide-sequence of a
RT gene encoding an acid-stable alpha-amylose from Aspergillus-
RT kawachi.";
RL J. Ferment. Bioeng. 81:292-298 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Kaneko A.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB008370; BAA22993.1; -.
DR HSSP; P56271; 2AAA.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_aml cat.
DR InterPro; IPR006589; Alp_aml cat sub.
DR InterPro; IPR002044; Glyco_hydro_CBD.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF00686; CBM_20; 1.
DR ProDom; PD001568; Glyco_hydro_CBD; 1.
DR SMART; SM00642; Aamy; 1.
SQ SEQUENCE 640 AA; 69507 MW; 676BF9D0236720DD CRC64;

Query Match 67.4%; Score 1810; DB 2; Length 640;
Best Local Similarity 67.6%; Pred. No. 1.9e-117;
Matches 325; Conservative 66; Mismatches 90; Indels 0; Gaps 0;

QY 18 ALAATPADWRSSQSIYFLITDRFARTDGTATCNTADOKYCGGTWQGIIDKLDYIQGMGF 77
Db 19 ALGLSAAEWRTQSIYFLITDRFRTDNTTATCNTGDQIYCGGSGQGIINHLDIYQGMGF 78
QY 78 TAIWITPTAQLPQTAYGDAYHYGWOQDIYSLNENYGTADDLKALSALHERGMVMD 137
Db 79 TAIWISPIEQLPQDTSDEAYHYGWOQKIYVNSNFGTADDLKSLSDALHARGMYLMD 138
QY 138 VVANHMGVDGAGSSVDYSVFPFSSQDYFHPFCFTQNTVEDQTVEDCWLGNTVSLPDL 197
Db 139 VVPNHMGVAGNGNDVYSVFPDFSSYFHPYCLITDNDLNTWQDCWEGDTIVSLPDLN 198
QY 198 TTKDVKVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCVGEVLDGPA 257
Db 199 TTETAVRIWYDWDVADLVSNYSVDGLRIDSVEEVEPDPFPQYQEAAGVYCVGEVDNGPA 258
QY 258 YTCPVQNVMDGVNLYPIYPLNAPKSTSGSMDDLYNNMINTVKS DCPDSTLLGTFFVENHD 317
Db 259 LDCPYQKYLGVNLYPIYQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHD 318
QY 318 NPFASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSE 377
Db 319 NPFASYTSDYSQAKNVLISFLSGIPIVYAGEEHYSGGVDGVPYNREATWLSGYDTSAE 378
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QY 378 LYKLIASANAI RNVAISKDTGFTVYKKNPIYKDDTTIAMRKGTGDSQIVTILSNKGASGD 437
Db 379 LYTWIATTNAIKLAISADSDYITKNDPIYDTSNTIAMRKGTSGSQIITVLSNKGSSGS 438
QY 438 SYTSLSGAGYTAGOOLTEVIGCTTIVTGVSGDNVVPVPMAGGLPRVLYPTEKLAGSKICSS 497
Db 439 SYTLTSLSGSGYTSGLTIEAVTCTSVTVDSNGDIPVPMASGLPRVLLPASVVVDSSSLCCG 498
QY 498 S 498
Db 499 S 499

RESULT 11
Q76L96
ID Q76L96 PRELIMINARY; PRT; 634 AA.
AC Q76L96;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Alpha-amylose precursor.
GN Name=amyl III;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=KT-11;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083162; BAD06005.1; -.
DR EMBL; AB083160; BAD06003.1; -.
DR HSSP; P04064; IACZ.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_aml cat.
DR InterPro; IPR006589; Alp_aml cat sub.
DR InterPro; IPR002044; Glyco_hydro_CBD.
DR Pfam; PF00128; Alpha-amylose; 1.
DR Pfam; PF00686; CBM_20; 1.
DR ProDom; PD001568; Glyco_hydro_CBD; 1.
DR SMART; SM00642; Aamy; 1.
KW Signal.
FT SIGNAL 1 21 Potential.
SQ SEQUENCE 634 AA; 69242 MW; 16C0BB6AF6FB0E9B CRC64;

Query Match 66.7%; Score 1791; DB 2; Length 634;
Best Local Similarity 68.6%; Pred. No. 3.9e-116;
Matches 321; Conservative 64; Mismatches 83; Indels 0; Gaps 0;

QY 18 ALAATPADWRSSQSIYFLITDRFARTDGTATCNTADOKYCGGTWQGIIDKLDYIQGMGF 77
Db 19 ALGLSAAEWRTQSIYFLITDRFRTDNTTATCNTGDQIYCGGSGQGIINHLDIYQGMGF 78
QY 78 TAIWITPTAQLPQTAYGDAYHYGWOQDIYSLNENYGTADDLKALSALHERGMVMD 137
Db 79 TAIWISPIEQLPQDTSDEAYHYGWOQKIYVNSNFGTADDLKSLSDALHARGMYLMD 138
QY 138 VVANHMGVDGAGSSVDYSVFPFSSQDYFHPFCFTQNTVEDQTVEDCWLGNTVSLPDL 197
Db 139 VVPNHMGVAGNGNDVYSVFPDFSSYFHPYCLITDNDLNTWQDCWEGDTIVSLPDLN 198
QY 198 TTKDVKVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCVGEVLDGPA 257
Db 199 TTETAVRIWYDWDVADLVSNYSVDGLRIDSVEEVEPDPFPQYQEAAGVYCVGEVDNGPA 258
QY 258 YTCPVQNVMDGVNLYPIYPLNAPKSTSGSMDDLYNNMINTVKS DCPDSTLLGTFFVENHD 317
Db 259 LDCPYQKYLGVNLYPIYQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHD 318
QY 318 NPFASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSE 377
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Db 319 NRPASYSQAKNVLSIFSLGDIPIVYAGEHQHSGDVPYNRATWLSGDTSAE 378
QY 378 LYKLIASANAIKRYAISKDTGFVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGD 437
Db 379 LVTWIAATNAIRKLAISADSDVITYANDPIYDNTSIAMRKGTSSQVITVLSNKGSSGS 438
QY 438 SYTSLSGAGYTAGOOLTEVICGTTVTGSDGNVPVPMAGGLPRVLYP 485
Db 439 SYTLTSGSGYTSGLTELIBAYTCTSVTVDSNGDIPVPMASGLPRVLLP 486

RESULT 12
ID AMYA ASPNG STANDARD; PRT; 484 AA.
AC P56271;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acid alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=91002514; PubMed=2207069;
RA Boel E., Brady L., Brzozowski A.M., Derewenda Z., Dodson G.G.,
RA Jensen V.J., Petersen S.B., Swift H., Thim L., Woldike H.F.;
RT "Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-
RT A resolution of two enzymes from Aspergillus.";
RL Biochemistry 29:6244-6249(1990).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
DR PDB; 2AAA; X-ray; @=1-484.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; Alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW 3D-structure; Calcium-binding; Carbohydrate metabolism; Glycoprotein;
KW Glycosidase; Hydrolase.
FT ACT_SITE 206 206 Nucleophile.
FT ACT_SITE 230 230 Proton donor.
FT ACT_SITE 297 297
FT METAL 121 121 Calcium 1.
FT METAL 162 162 Calcium 1 (via carbonyl oxygen).
FT METAL 175 175 Calcium 1.
FT METAL 206 206 Calcium 2.
FT METAL 210 210 Calcium 1 (via carbonyl oxygen).
FT METAL 230 230 Calcium 2.
FT DISULFID 30 38
FT DISULFID 150 164
FT DISULFID 240 283
FT DISULFID 440 475
FT CARBOHYD 24 24 N-linked (GlcNAc.. ) (Potential).
FT CARBOHYD 157 157 N-linked (GlcNAc.. ) (Potential).
FT CARBOHYD 197 197 N-linked (GlcNAc.. ) (Potential).
FT HELIX 3 6
FT TURN 7 8
FT STRAND 11 13
FT HELIX 16 19
FT TURN 22 23
FT HELIX 32 34
FT HELIX 42 47
FT TURN 48 48
FT HELIX 49 53
FT TURN 54 56
FT STRAND 59 62
FT STRAND 66 68

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Query Match

66.2%; Score 1778; DB 1; Length 484;
 484 AA; 52935 MW; 04D596E34680656D CRC64;

Best Local Similarity 66.9%; Pred. No. 2.2e-115;
Matches 318; Conservative 63; Mismatches 94; Indels 0; Gaps 0;

QY	24	ADWRSOSIFLLTDRFARTDGS	TATCNTADQKYCGGTWQGIIDKLDYIQMGFTAIWIT	83
Db	4	ASWRTQSIFLLTDRFRTDNT	TATCNTNEIYCGSGWQGIIDHLDYIEGFGTAIWIS	63
QY	84	PVTAQLPQTAYGDAYHYGQQD	IYSLNENYGTADDLKALSSALHARGMYLMDVVANHM	143
Db	64	PIEQLPQDTADGEAYHYGQQI	YDVNSNFGTADNLKSLSDALHARGMYLMDVVDPDM	123
QY	144	GYDGAGSSVDYSVFKPSSQD	YHPHPCFTQNTVEDQVDEDCWLGNTVSLPDLDTTKDVV	203
Db	124	GYAGNGNDVSYFDFPSSYPH	PHYCLITDMDNLTMWEDCWEGDTIVSLPDLDTTETAV	183
QY	204	KNESWDVWGLSVNSYIDGLR	IDTVKHVKQDFWPGYNKAAGVYCTGEVLDDGPAYTCYQ	263
Db	184	RTIYDWDVADLVNSYVSDGLR	IDSLEVDQDFPFGYNKASGYCGEIDNGNPASDCPYQ	243
QY	264	NVMDGVLNPIYIYPLLNAFK	STSGMDDLNNMINTVKSDCPDSTLLGTFFVENHNDPRFAS	323
Db	244	KVLDDVLNPIYQWLLYAFES	SGSISLNNYIKSVASDCSDPTLLGNFIENHNDPRFAK	303
QY	324	YTDIALAKNVAFIILNDGIP	IPIYAGQOHVAGNDPANREATWLSGYPTDSELYKLLIA	383
Db	304	YTSYDQAKNLVSIYFLSDG	IPIVYAGEQHVGKVPYNREATWLSGYDTSAELYTWIA	363
QY	384	SANAINYALSKDTGFVYKN	PIYKDDTTIAMRGTGDSQIIVTILSNKSGDSYTLSL	443
Db	364	TTNAIRKLAADSAVATYI	ANDAFYDNTIAWAKTSGSVITVLSNKGSGGSYTLTL	423
QY	444	SGAGYTAGOOLTTEVIGCT	TTVTGVSGDNVPMVPMAGGLPRVLYPTEKLAGSKICSSS	498
Db	424	SGSGYTSGLKLIBEAYTCT	SVTVDDSSGDIIVPMASGLPRVLLPASVVDSSSLCGGS	478

RESULT 13

ID	Q9UV09	PRELIMINARY;	PRT;	623 AA.
AC	OSUV09;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Alpha-amylase.			
DE	Name=amvB;			
GN	Emericella nidulans (Aspergillus nidulans).			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;			
OC	Eurotiales; Trichocomaceae; Emericella.			
OX	NCBI_TaxID=162425;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Boase N.A., Murphy R.L., Kelly J.M.;			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.			
DR	EMBL; AF208224; AAF17100.1; -			
DR	HSSP; P56271; 2AAA.			
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.			
DR	GO; GO:0003924; P:catalytic activity; IEA.			
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro; IPR006047; Alpha_amyl_cat.			
DR	InterPro; IPR006047; Alpha_cat_sub.			
DR	InterPro; IPR002044; Glyco_hydro_13.			
DR	InterPro; IPR002044; Glyco_hydro_CBD.			
DR	Pfam; PF00128; Alpha-amylase; 1.			
DR	Pfam; PF00686; CBM_20; 1.			
DR	PRINTS; PR00110; ALPHAAMYLASE.			
DR	ProDom; PD001568; Glyco_hydro_CBD; 1.			
DR	SMART; SM00642; Aamy; 1.			
SQ	SEQUENCE 623 AA; 68598 MW; 822F002C37F5A9A4 CRC64;			

Query Match 64.3%; Score 1725.5; DB 2; Length 623;
Best Local Similarity 63.7%; Pred. No. 1.4e-111;
Matches 309; Conservative 68; Mismatches 107; Indels 1; Gaps 1;

QY	12	LQVAAAPALAAATPAD-WRSQ	SIYFLLTDRFARTDGS	TATCNTADQKYCGGTWQGIIDKLD	70
Db	10	LALLGKAVHGLDADGWSQSI	YFLLTDRFARTDGS	TAAACDLAQRYYCGSGWQGIINQLD	69
QY	71	YIQMGFTAIWITPVTAQLPQT	AYGDAYHYGQQDIYSLNENY	GTADDLKALSSALHARGMYLMD	130
Db	70	YIQMGFTAIWITPITEQIPDV	TAVGTGFHYWQKNIYVD	TNLGTADDIRALSEALHADR	129
QY	131	GMYLMDVWVANHMGYDAGS	SDYSVFKPSSQDYHPHPCF	IONYEDQVDEDCWLGNDNT	190
Db	130	GMYLMDVWVANHMSYGGP	SGSTDFSITPPDSASYFHSY	CAINNYDNQWQVENCFLGDDT	189
QY	191	VSLPDLDTTKVKNENYDMV	GLSVNSYIDGLRIDTVKHVK	QDFWPGYNKAAGVYCTGEV	250
Db	190	VSLTDLNTQSSSEVRDIW	DMIEDIVANSYDGLRIDTV	KHVEKDFWPGYIDAAGVYSVG	249
QY	251	VLDGDPAYTCPYQNVMDG	VLNPIYIYPLLNAFKSTSG	MDDLNNMINTVKSDCPDSTLLG	310
Db	250	IFHGDPAITCPYQDYMDG	VNPIYIYPLLNAFKSSGS	SDLSNNTVSNKSGGSQVLTLLG	309
QY	311	TFVENHNDPRFASVTDIAL	AKNVAFIILNDGIP	IPIYAGQOHVAGNDPANREATWLS	370
Db	310	NFTENHNDPRFPNYP	TPDMSRAKNVLAFLT	DTGDIPIYAGQOHYSGSNDPYNR	369
QY	371	GYPTDSELYKLIASAINR	YALSKDTGFVYKNPIYKDD	TTIAMRGTGDSQIIVTILS	430
Db	370	SYSTSSELYKFIATNTKIR	KLAIKSDSYLTSTNT	PFYSDSNYIAMRKGSGGSQVLTLLN	429
QY	431	NKAGSDSYTSLISGAGYTA	GOOLTTEVIGCTTVTGVSG	DNVPMVPMAGGLPRVLYPTEKLA	490
Db	430	NIGTSGSYTFDLYHDYH	GSANLVELYTCSSVQVGS	NGAISIPMTSGLPVLPVPAWVS	489
QY	491	GSKIC 495			
Db	490	GSGLC 494			

RESULT 14

QY	Q6YF33	PRELIMINARY;	PRT;	647 AA.
AC	Q6YF33			

Query Match	64.3%;	Score 1725.5;	DB 2;	Length 623;
Best Local Similarity	63.7%;	Pred. No. 1.4e-111;		
Matches 309; Conservative	68;	Mismatches 107;	Indels 1;	Gaps 1;
Query Match	61.9%;	Score 1662;	DB 2;	Length 647;
Best Local Similarity	61.4%;	Pred. No. 3.8e-107;		
Matches 309; Conservative	68;	Mismatches 107;	Indels 1;	Gaps 1;
SQ SEQUENCE	647 AA;	70957 MW;	D94607IDB/560144	CRC64;

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Matches 298; Conservative 75; Mismatches 110; Indels 2; Gaps 1;
QY 12 LQVAAALAAATPADWRSQSIYFLLRDTPARTDGTATCNADQKCGTQWQGIIDKLDY 71
Db 164 ISVSV--TGAANWGRRAIQVITDRFARTDGTITLCLDVTDRVYCGGSIQGINNLDY 221
QY 72 IQMGFTAIWTPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDLKALSSALHREG 131
Db 222 IQMGFTAIWISPIVENIPDDTGYGAYHGYWMDIFALNTNFGTADDLIALATELHNRG 281
QY 132 MYLMDVIVNHNHAFSGHADVDYSEYFPYSSQDYFHSFCWITDYSQNTNVEQCMGDDIV 191
Db 282 MYLMDVIVNHNHAFSGHADVDYSEYFPYSSQDYFHSFCWITDYSQNTNVEQCMGDDIV 341
QY 192 SLPDLTDDKVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAAGVYICGEV 251
Db 342 PLVDVNTQLDVTKSEYQSWQELIANYSIDGLRIDTVKHVQKDFWPAQEAAGIYAVGEV 401
QY 252 LDGDPATPCYQNVMDGLNRYPIYPLNFAKSTSGSMDLNNMINTVKSDCPDSTLLGT 311
Db 402 FDGDPSTPCYQNLGVLNYPYIPVSAFESVSGSVSLVMDITLXSECTDITLLGS 461
QY 312 FVENHNPFPASYNIDIALAKNAFAFIILNDGIPPIYAGQEHYAGGNDPANREATWLSG 371
Db 462 FLENQNPFPSTVDSLEIKNAIAFTMLSDGPIIYQGEQGLNGNDPYNREALWLIG 521
QY 372 YPTDSLYKLJASANAIRNVAISKOTGFVYKNWPIYKDDTTIAMRGDGTGQIVTILSN 431
Db 522 YSTSTFYKYIASLQIRNAIQKDDTYLTQYQNWIVYSDSTTIAMRGKTGNQIIVLSN 581
QY 432 KGAGSDSYTSLSGAGYTAGQQLTEVIGCTTVYVSGDGNVPVPMAGLPRVLYPTKLAG 491
Db 582 LGTSGSSYTLTSLNTGTASSVVYELTCTAVTVDSGNLAVPMSSGLPKVYQESQLVG 641
QY 492 SKICS 496
Db 642 SGICS 646

RESULT 15
AMYL LIPKO
ID AMYL LIPKO STANDARD; PRT; 624 AA.
AC Q0117;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase 1).
GN Name=LXAI;
OS Lipomyces kononenkoae.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Lipomycetaceae; Lipomyces.
OX NCBI_TaxID=34357;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IGC4052B;
RA MEDLINE=96105202; PubMed=8529895; DOI=10.1016/0378-1119(95)00633-0;
RX Steyn A.J.C., Marmur J., Pretorius I.S.;
RT "Cloning, sequence analysis and expression in yeasts of a CDNA
RT containing a Lipomyces kononenkoae alpha-amylase-encoding gene.";
RL Gene 166:65-71(1995).
RN [2]
RP SEQUENCE OF 29-44.
RC STRAIN=IGC4052B;
RX MEDLINE=96132108; PubMed=8593683;
RA Steyn A.J.C., Pretorius I.S.;
RT "Characterization of a novel alpha-amylase from Lipomyces kononenkoae
RT and expression of its gene (lXAI) in Saccharomyces cerevisiae.";
RL Curr. Genet. 28:526-533(1995).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
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CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -1- SIMILARITY: Contains 1 carbohydrate binding type-21 (CBM21)
CC domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; U30376; AAC49622.1; ALT_INIT.
DR PIR; JC4510; JC4510.
DR HSP; P10529; 7TAA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR005036; CBM_21.
DR Pfam; PF00128; Alpha-amylase; 1.
DR Pfam; PF03370; CBM_21; 1.
DR SMART; SM00642; Amy; 1.
DR KEGG; K01000; Amy; 1.
KW Calcium-binding; Carbohydrate metabolism; Direct protein sequencing;
KW Glycoprotein; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 28
FT CHAIN 29 624 Alpha-amylase 1.
FT DOMAIN 40 133 Carbohydrate binding type-21.
FT ACT_SITE 353 353 Nucleophile (By similarity).
FT ACT_SITE 377 377 Proton donor (By similarity).
FT ACT_SITE 444 444 By similarity.
FT METAL 268 268 Calcium 1 (By similarity).
FT METAL 309 309 Calcium 1 (via carbonyl oxygen) (By
FT similarity).
FT METAL 322 322 Calcium 1 (By similarity).
FT METAL 353 353 Calcium 2 (By similarity).
FT METAL 357 357 Calcium 1 (via carbonyl oxygen) (By
FT similarity).
FT METAL 377 377 Calcium 2 (By similarity).
FT DISULFID 177 185 By similarity.
FT DISULFID 297 311 By similarity.
FT DISULFID 387 430 By similarity.
FT DISULFID 587 622 By similarity.
FT CARBOHYD 304 304 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 344 344 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 624 AA; 68876 MW; 87EB16534F5A9A9F CRC64;

Query Match 60.7%; Score 1629; DB 1; Length 624;
Best Local Similarity 60.6%; Pred No. 7.1e-105;
Matches 292; Conservative 77; Mismatches 113; Indels 0; Gaps 0;

QY 15 AAPALAAATPADWRSQSIYFLLRDTPARTDGTATCNADQKCGTQWQGIIDKLDYIQG 74
Db 142 SASVPTGAANWGRSIYQVVTDRFARTDGTITLCLDVTDRVYCGGSIQGINNLDYIQG 201
QY 75 MGFTAIWTPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDLKALSSALHREGMYL 134
Db 202 MGFTAIWISPIVENIPDDTGYGAYHGYWMDIFALNTNFGTADDLIALATELHNRGMYL 261
QY 135 MYDVVANMGYDAGSSVDYSVFKPSSQDYFHSFCWITDYSQNTNVEQCMGDDIVSLP 194
Db 262 MYDIVNHFASFNGHADVDYSEYFPYSSQDYFHSFCWITDYSQNTNVEQCMGDDIVSLP 321
QY 195 DLDTTKDVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAAGVYICGEVLIDG 254
Db 322 DVNTQLDVTKSEYQSWQELIANYSIDGLRIDTVKHVQKDFWPAQEAAGIYVGEVFDG 381
QY 255 DPATYCPQNVMDGLNRYPIYPLNFAKSTSGSMDLNNMINTVKSDCPDSTLLGTFFVB 314
Db 382 DPSYTCYQNLGVLNYPYIPVSAFESVSGSVSLVMDITLXSECTDITLLGSFFLE 441
QY 315 NHDNPRFPASYNIDIALAKNAFAFIILNDGIPPIYAGQEHYAGGNDPANREATWLSGYPT 374
Db 442 NODNPRFPSTVDSLEIKNAIAFTILSDGIPPIIYQGEQGLNGNDPYNREALWPTGYST 501
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OM protein - protein search, using sw model

Run on: November 7, 2005, 17:47:24 ; Search time 74.9884 Seconds
(without alignments)
495.746 Million cell updates/sec

Title: US-10-820-200-2

Perfect score: 2684

Sequence: 1 MWAWSLFLYGLQVAAPALA.....LPRVLYPTKLAGSKICSSS 498

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents 'AA':*

- 1: /cgn2_6/protdata/1/1aa/5A COMB pep:*
- 2: /cgn2_6/protdata/1/1aa/5B COMB pep:*
- 3: /cgn2_6/protdata/1/1aa/6A COMB pep:*
- 4: /cgn2_6/protdata/1/1aa/6B COMB pep:*
- 5: /cgn2_6/protdata/1/1aa/PCITUS COMB pep:*
- 6: /cgn2_6/protdata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2572	95.8	478	1	US-08-720-899-7
2	2572	95.8	478	1	US-08-459-610-7
3	2572	95.8	478	2	US-08-343-804-7
4	2572	95.8	478	2	US-08-600-908A-10
5	2572	95.8	478	3	US-08-683-838A-10
6	2572	95.8	478	3	US-09-182-859-7
7	2572	95.8	478	4	US-09-672-459-7
8	2572	95.8	478	4	US-09-636-252A-10
9	2572	95.8	478	4	US-10-186-042-7
10	2503.5	93.3	478	2	US-08-339-715A-2
11	1392	51.9	468	1	US-08-470-702-6
12	1392	51.9	468	1	US-08-467-831-6
13	1391	51.8	468	1	US-08-204-656B-4
14	1391	51.8	468	1	US-08-470-702-7
15	1391	51.8	468	1	US-08-467-831-7
16	1388	51.7	468	1	US-08-204-656B-6
17	1388	51.7	468	1	US-08-470-702-8
18	1388	51.7	468	1	US-08-467-831-8
19	1387	51.7	468	1	US-08-204-656B-2
20	1387	51.7	468	1	US-08-204-656B-8
21	1387	51.7	468	1	US-08-470-702-9
22	1387	51.7	468	1	US-08-467-831-9
23	450	16.8	719	3	US-09-386-607-2
24	450	16.8	719	3	US-09-645-707B-2
25	446	16.6	686	3	US-08-947-965-73
26	444	16.5	685	3	US-08-947-965-72
27	428.5	16.0	655	1	US-08-469-202-28

28	428.5	16.0	655	2	US-08-484-434C-35	Sequence 35, Appl
29	428.5	16.0	655	4	US-09-384-361-35	Sequence 35, Appl
30	427.5	15.9	655	1	US-08-469-202-27	Sequence 27, Appl
31	427.5	15.9	655	2	US-08-484-434C-34	Sequence 34, Appl
32	427.5	15.9	655	4	US-09-384-361-34	Sequence 34, Appl
33	426.5	15.9	683	3	US-08-947-965-2	Sequence 2, Appl
34	421.5	15.7	624	3	US-08-947-965-78	Sequence 78, Appl
35	418	15.6	676	3	US-08-947-965-71	Sequence 71, Appl
36	413	15.4	686	3	US-08-947-965-70	Sequence 70, Appl
37	413	15.4	687	3	US-08-947-965-75	Sequence 75, Appl
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39	404.5	15.1	833	4	US-10-014-436-3	Sequence 3, Appl
40	404.5	15.1	1938	3	US-09-514-302-2	Sequence 2, Appl
41	404.5	15.1	1938	4	US-10-014-436-2	Sequence 2, Appl
42	398	14.8	685	3	US-08-947-965-74	Sequence 74, Appl
43	396	14.8	675	3	US-08-947-965-76	Sequence 76, Appl
44	385.5	14.4	680	3	US-08-947-965-77	Sequence 77, Appl
45	370	13.8	588	2	US-08-339-715A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-08-720-899-7
; Sequence 7, Application US/08720899
; Patent No. 5753460
; GENERAL INFORMATION:
; APPLICANT: Biesgaard-Frantzen, Henrik
; APPLICANT: Borchart, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57534600 No. 5753460disk of No. 5753460th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,899
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Query Match 95.8%; Score 2572; DB 1; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 21 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKYCGGTWQGIIDKLDIYIQGMGFTAI 80
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Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKYCGGTWQGIIDKLDIYIQGMGFTAI 60
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QY 81 WITPVTQAQLPQTAYGDAYHGHWQODIYSLNENYGTADDLKSALHERGMYLMDVVA 140
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QY 261 PYQNVMDGVLNYPYIYPLLNAPKSTSGSMDLLYNMINTVKSDCPDSTLLGTFFVENHNDNPR 320
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Db 241 PYQNVMDGVLNYPYIYPLLNAPKSTSGSMDLLYNMINTVKSDCPDSTLLGTFFVENHNDNPR 300
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QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYVAGGNDPANREATWLSGYPTDSELYK 380
| | | | |
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYVAGGNDPANREATWLSGYPTDSELYK 360
| | | | |
QY 381 LIASANAIRNVAIAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIIVTILSNKGASGDSYT 440
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Db 361 LIASANAIRNVAIAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIIVTILSNKGASGDSYT 420
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QY 441 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 498
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Db 421 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 478
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RESULT 2

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US-08-459-610-7
; Sequence 7, Application US/08459610
; Patent No. 5801043
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5801043o No. 5801043disk of No. 5801043th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,610
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-459-610-7

Query Match          95.8%; Score 2572; DB 1; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKYCGGTWQGIIDKLDIYIQGMGFTAI 80
| | | | |
Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKYCGGTWQGIIDKLDIYIQGMGFTAI 60
| | | | |
QY 81 WITPVTQAQLPQTAYGDAYHGHWQODIYSLNENYGTADDLKSALHERGMYLMDVVA 140
| | | | |
Db 61 WITPVTQAQLPQTAYGDAYHGHWQODIYSLNENYGTADDLKSALHERGMYLMDVVA 120
| | | | |
QY 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVQEDCWLGDNVTSLPDLDTTK 200
| | | | |
Db 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVQEDCWLGDNVTSLPDLDTTK 180
| | | | |
QY 201 DVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGYVCIGEVLDGDPAYTC 260
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Db 181 DVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGYVCIGEVLDGDPAYTC 240
| | | | |
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Db 241 PYQNVMDGVLNYPYIYPLLNAPKSTSGSMDLLYNMINTVKSDCPDSTLLGTFFVENHNDNPR 300
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Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYVAGGNDPANREATWLSGYPTDSELYK 360
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QY 381 LIASANAIRNVAIAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIIVTILSNKGASGDSYT 440
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Db 361 LIASANAIRNVAIAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIIVTILSNKGASGDSYT 420
| | | | |
QY 441 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 498
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Db 421 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 478
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RESULT 3
US-08-343-804-7
; Sequence 7, Application US/08343804
; Patent No. 5830837
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5830837o No. 5830837disk of No. 5830837th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,804
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
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REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-343-804-7

Query Match 95.8%; Score 2572; DB 2; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGTTCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 80
DB 1 ATPADWRSQSIYFLLTDRFARTDGTTCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTALPQTAYGDAYHGYWQDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
DB 61 WITPVTALPQTAYGDAYHGYWQDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120
QY 141 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFTONYEDQTVEDCWLGDNVSLPDLDTTK 200
DB 121 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFTONYEDQTVEDCWLGDNVSLPDLDTTK 180
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DB 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGELVDGDPAYTC 240
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DB 241 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKSDCPSTLLGTTFVENHNDPR 300
QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSSELYK 380
DB 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSSELYK 360
QY 381 LIASANAIRNVAISKDTGFVTKNWPYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 440
DB 361 LIASANAIRNVAISKDTGFVTKNWPYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 420
QY 441 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPPVPMAGGLPRVLYPTEKLAGSKICSSS 498
DB 421 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPPVPMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 4
US-08-600-908A-10
Sequence 10, Application US/08600908A
Patent No. 5989169
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Prantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5989169 No. 5989169disk of No. 5989169th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/600,908A
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-600-908A-10

Query Match 95.8%; Score 2572; DB 2; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGTTCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 80
DB 1 ATPADWRSQSIYFLLTDRFARTDGTTCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTALPQTAYGDAYHGYWQDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
DB 61 WITPVTALPQTAYGDAYHGYWQDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120
QY 141 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFTONYEDQTVEDCWLGDNVSLPDLDTTK 200
DB 121 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFTONYEDQTVEDCWLGDNVSLPDLDTTK 180
QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGELVDGDPAYTC 260
DB 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGELVDGDPAYTC 240
QY 261 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKSDCPSTLLGTTFVENHNDPR 320
DB 241 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKSDCPSTLLGTTFVENHNDPR 300
QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSSELYK 380
DB 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSSELYK 360
QY 381 LIASANAIRNVAISKDTGFVTKNWPYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 440
DB 361 LIASANAIRNVAISKDTGFVTKNWPYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 420
QY 441 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPPVPMAGGLPRVLYPTEKLAGSKICSSS 498
DB 421 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPPVPMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 5
US-08-683-838A-10
Sequence 10, Application US/08683838A
Patent No. 6022724
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Prantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6022724 No. 6022724disk of No. 6022724th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,838A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/600,908
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-683-838A-10

Query Match 95.8%; Score 2572; DB 3; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 ATPADWRSQSIYFLITDRFARTDGSSTTATCNADQKCGGTWQGIIDKLDYIQMGFTAI 80
Db 1 ATPADWRSQSIYFLITDRFARTDGSSTTATCNADQKCGGTWQGIIDKLDYIQMGFTAI 60
QY 81 WITPVTAQLPQTAYGDAYHGHWQDIYSLNENYGTADDLKSALHERGMYLMDVVA 140
Db 61 WITPVTAQLPQTAYGDAYHGHWQDIYSLNENYGTADDLKSALHERGMYLMDVVA 120
QY 141 NHMGVDGAGSSVDYVFKPFSSQDYFHPFCFIONYEDQTVEDCWLGDNVSLPLDITTK 200
Db 121 NHMGVDGAGSSVDYVFKPFSSQDYFHPFCFIONYEDQTVEDCWLGDNVSLPLDITTK 180
QY 201 DVVKNEDWVGSLVSNYSIDGLRDTVKHVKQDFWPGYNKAAGVYCI GEVLGDGPATC 260
Db 181 DVVKNEDWVGSLVSNYSIDGLRDTVKHVKQDFWPGYNKAAGVYCI GEVLGDGPATC 240
QY 261 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDPR 320
Db 241 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDPR 300
QY 321 FASYTNDIALAKNVAFAFIINDGIPIIYAGQHQYAGGNDPANREATWLSGYPTDSLEYK 380
Db 301 FASYTNDIALAKNVAFAFIINDGIPIIYAGQHQYAGGNDPANREATWLSGYPTDSLEYK 360
QY 381 LIASANAIRNVAISKDTGFVTKWPIYKDDTTIAMRKGTGDSOIIVTILSNKGASGDSYT 440
Db 361 LIASANAIRNVAISKDTGFVTKWPIYKDDTTIAMRKGTGDSOIIVTILSNKGASGDSYT 420
QY 441 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSS 498
Db 421 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSS 478

RESULT 6
US-09-182-859-7
Sequence 7, Application US/09182859
Patent No. 6143708
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen, Henrik

TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/182,859
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 0515/96
EARLIER FILING DATE: 1996-04-30
EARLIER APPLICATION NUMBER: 0712/96
EARLIER FILING DATE: 1996-06-28
EARLIER APPLICATION NUMBER: 0775/96
EARLIER FILING DATE: 1996-07-11
EARLIER APPLICATION NUMBER: 1263/96
EARLIER FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 478
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-182-859-7
Query Match 95.8%; Score 2572; DB 3; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 ATPADWRSQSIYFLITDRFARTDGSSTTATCNADQKCGGTWQGIIDKLDYIQMGFTAI 80
Db 1 ATPADWRSQSIYFLITDRFARTDGSSTTATCNADQKCGGTWQGIIDKLDYIQMGFTAI 60
QY 81 WITPVTAQLPQTAYGDAYHGHWQDIYSLNENYGTADDLKSALHERGMYLMDVVA 140
Db 61 WITPVTAQLPQTAYGDAYHGHWQDIYSLNENYGTADDLKSALHERGMYLMDVVA 120
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Db 121 NHMGVDGAGSSVDYVFKPFSSQDYFHPFCFIONYEDQTVEDCWLGDNVSLPLDITTK 180
QY 201 DVVKNEDWVGSLVSNYSIDGLRDTVKHVKQDFWPGYNKAAGVYCI GEVLGDGPATC 260
Db 181 DVVKNEDWVGSLVSNYSIDGLRDTVKHVKQDFWPGYNKAAGVYCI GEVLGDGPATC 240
QY 261 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDPR 320
Db 241 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDPR 300
QY 321 FASYTNDIALAKNVAFAFIINDGIPIIYAGQHQYAGGNDPANREATWLSGYPTDSLEYK 380
Db 301 FASYTNDIALAKNVAFAFIINDGIPIIYAGQHQYAGGNDPANREATWLSGYPTDSLEYK 360
QY 381 LIASANAIRNVAISKDTGFVTKWPIYKDDTTIAMRKGTGDSOIIVTILSNKGASGDSYT 440
Db 361 LIASANAIRNVAISKDTGFVTKWPIYKDDTTIAMRKGTGDSOIIVTILSNKGASGDSYT 420
QY 441 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSS 498
Db 421 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSS 478
RESULT 7
US-09-672-459-7
Sequence 7, Application US/09672459
Patent No. 6436888
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/672,459
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30

;; PRIOR APPLICATION NUMBER: 0712/96
;; PRIOR FILING DATE: 1996-06-28
;; PRIOR APPLICATION NUMBER: 0775/96
;; PRIOR FILING DATE: 1996-07-11
;; PRIOR APPLICATION NUMBER: 1263/96
;; PRIOR FILING DATE: 1996-11-08
;; NUMBER OF SEQ ID NOS: 37
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 7
;; LENGTH: 478
;; TYPE: PR1
;; ORGANISM: Bacillus licheniformis
US-09-672-459-7

Query Match 95.8%; Score 2572; DB 4; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNYAISKDTGFVYKNWPIYKDDITIAMRKGTGDSQIVTILSNKGASGDSYT 440
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QY 441 LSLSGAGYTAGQQLTEVIGCTTTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
Db 421 LSLSGAGYTAGQQLTEVIGCTTTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 8
US-09-636-252A-10
;; Sequence 10, Application US/09636252A
;; Patent No. 6440716
;; GENERAL INFORMATION:
;; APPLICANT: Svendsen, Allan
;; APPLICANT: Bisgard-Frantzen, Henrik
;; APPLICANT: Borchert, Torben Vedel
;; TITLE OF INVENTION: Alpha-Amylase Mutants
;; FILE REFERENCE: 0776/1F216-US2
;; CURRENT APPLICATION NUMBER: US/09/636, 252A
;; PRIOR FILING DATE: 2000-08-10
;; PRIOR APPLICATION NUMBER: 08/683, 838
;; PRIOR FILING DATE: 1996-07-18
;; NUMBER OF SEQ ID NOS: 16
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 10
;; LENGTH: 478
;; TYPE: PR1
;; ORGANISM: A. oryzae
US-09-636-252A-10

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Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 360
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Db 361 LIASANAIRNYAISKDTGFVYKNWPIYKDDITIAMRKGTGDSQIVTILSNKGASGDSYT 420
QY 441 LSLSGAGYTAGQQLTEVIGCTTTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
Db 421 LSLSGAGYTAGQQLTEVIGCTTTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 9
US-10-186-042-7
;; Sequence 7, Application US/10186042
;; Patent No. 6642044
;; GENERAL INFORMATION:
;; APPLICANT: Svendsen, Allan
;; APPLICANT: Borchert, Torben
;; APPLICANT: Bisgard-Frantzen, Henrik
;; TITLE OF INVENTION: Alpha-Amylase Mutants
;; FILE REFERENCE: 4796.204-US
;; CURRENT APPLICATION NUMBER: US/10/186, 042
;; PRIOR FILING DATE: 2002-06-28
;; PRIOR APPLICATION NUMBER: US/09/672, 459
;; PRIOR FILING DATE: 2000-09-28
;; PRIOR APPLICATION NUMBER: 09/182, 859
;; PRIOR FILING DATE: 1998-10-29
;; PRIOR APPLICATION NUMBER: 0515/96
;; PRIOR FILING DATE: 1996-04-30
;; PRIOR APPLICATION NUMBER: 0712/96
;; PRIOR FILING DATE: 1996-06-28
;; PRIOR APPLICATION NUMBER: 0775/96
;; PRIOR FILING DATE: 1996-07-11
;; PRIOR APPLICATION NUMBER: 1263/96
;; PRIOR FILING DATE: 1996-11-08
;; NUMBER OF SEQ ID NOS: 37
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 7
;; LENGTH: 478
;; TYPE: PR1
;; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match 95.8%; Score 2572; DB 4; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/470, 702
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/204,656
; FILING DATE: 02-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-470-702-6

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Matches 259; Conservative 81; Mismatches 126; Indels 10; Gaps 5;

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DB 62 WISPVVENIPDNTAYGYAHGFWMKNYIKENYFGTADDLKSALSHRGMVLMVDVIVT 121

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DB 242 PYQNYIPGVSNYPLYIYPTTRPFTTDSSELSQTMISSVASSCSDPTLLTNFVENHDNR 301

QY 321 FASYTNDIALAKNVAAPFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 380
DB 302 FASMTSDQSLISNAIAFVLLGDGIPVIYVYQEGQLSGKSDPNNREALWLSGYNKESDYK 361

QY 381 LIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKGTDSQIVTILSNKGASDST 440
DB 362 LIAKANAARNAAVYQSSVATSLQSVIFSNHDVIAIKRGS----VVSFNNLSSGSS-D 416

QY 441 LSLSGAGYTAGOOLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICS 496
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RESULT 12
US-08-467-831-6
; Sequence 6, Application US/08467831
; Patent No. 5635378
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKUO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
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OM protein - protein search, using sw model

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Scoring table: BLOSUM62

Searched: 1867879 seqs, 418409474 residues

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Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	2674	99.6	499	16	US-10-877-849-36
7	2662	99.2	498	16	US-10-815-495-18
8	2572	95.8	478	14	US-10-815-495-22
9	2572	95.8	478	14	US-10-184-771-10
10	2572	95.8	478	14	US-10-186-042-7
11	2572	95.8	478	15	US-10-644-187-7
			478	17	US-10-926-720-10

12	2572	95.8	478	17	US-10-980-759-7	Sequence 7, Appli
13	2572	95.8	478	20	US-11-064-196-10	Sequence 10, Appl
14	2570	95.8	476	17	US-10-877-849-43	Sequence 43, Appl
15	2569	95.7	1095	14	US-10-228-063-45	Sequence 45, Appl
16	2100	78.2	495	14	US-10-213-990-42	Sequence 42, Appl
17	2012	75.0	494	17	US-10-486-868-13	Sequence 13, Appl
18	1835	68.4	630	14	US-10-213-990-45	Sequence 45, Appl
19	1810	67.4	640	17	US-10-877-007-22	Sequence 22, Appl
20	1810	67.4	640	17	US-10-877-849-41	Sequence 41, Appl
21	1798	67.0	505	17	US-10-877-849-42	Sequence 42, Appl
22	1798	67.0	511	17	US-10-877-849-8	Sequence 8, Appli
23	1798	67.0	609	17	US-10-877-849-38	Sequence 38, Appl
24	1798	67.0	629	17	US-10-877-849-34	Sequence 34, Appl
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26	1778	66.2	484	15	US-10-416-393-1	Sequence 1, Appli
27	1778	66.2	484	16	US-10-797-393A-1	Sequence 18, Appl
28	1214.5	45.2	547	14	US-10-213-990-48	Sequence 48, Appl
29	1183	44.1	555	17	US-10-486-868-15	Sequence 15, Appl
30	1163	43.3	567	17	US-10-486-868-18	Sequence 18, Appl
31	1160	43.2	500	15	US-10-369-493-12469	Sequence 12469, A
32	1085	40.4	549	17	US-10-486-868-14	Sequence 14, Appl
33	1015.5	37.8	513	15	US-10-369-493-2223	Sequence 2223, Ap
34	898.5	33.5	564	15	US-10-369-493-22679	Sequence 22679, A
35	873	32.5	493	15	US-10-369-493-22723	Sequence 22723, A
36	651	24.3	263	16	US-10-435-115-291647	Sequence 291647,
37	541	20.2	502	14	US-10-081-872-108	Sequence 108, App
38	541	20.2	502	15	US-10-385-305-108	Sequence 108, App
39	483.5	18.0	547	15	US-10-369-493-19940	Sequence 19940, A
40	480.5	17.9	547	15	US-10-369-493-19062	Sequence 19062, A
41	456.5	17.0	713	17	US-10-504-543-4	Sequence 4, Appli
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43	450	16.8	719	15	US-10-442-558-2	Sequence 2, Appli
44	450	16.8	719	15	US-10-453-828-2	Sequence 2, Appli
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ALIGNMENTS

RESULT 1
US-10-820-200-2
; Sequence 2, Application US/10820200
; Publication No. US20040229764A1
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Pedersen, Sven
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
; FILE REFERENCE: 5835.200-US
; CURRENT APPLICATION NUMBER: US/10/820,200
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US/09/710,339
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/165,786
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus Oryzae
US-10-820-200-2

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Qy 241 KAAGVYCI GEVLGDGPAYTCYQNVMDGVNLNPIYPLNAPKSTSGSMDDLNNINTVK 300
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; Sequence 30, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
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; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-877-849-30

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Qy 241 KAAGVYCI GEVLGDGPAYTCYQNVMDGVNLNPIYPLNAPKSTSGSMDDLNNINTVK 300
Db 241 KAAGVYCI GEVLGDGPAYTCYQNVMDGVNLNPIYPLNAPKSTSGSMDDLNNINTVK 300
Qy 301 SDPCDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGQSOHYAGGND 360
Db 301 SDPCDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGQSOHYAGGND 360
Qy 361 PANREATWLSGYPDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRGT 420
Db 361 PANREATWLSGYPDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRGT 420
Qy 421 DGSQIVTILSNKGAGSDSYTILSLGAGYTAGQQLTEVIGCTTIVTSGDGNVVPVPMAGGLP 480
Db 421 DGSQIVTILSNKGAGSDSYTILSLGAGYTAGQQLTEVIGCTTIVTSGDGNVVPVPMAGGLP 480
Qy 481 RVLVPTTEKLAGSKICSSS 498
Db 481 RVLVPTTEKLAGSKICSSS 498
RESULT 3
US-10-797-393A-5
; Sequence 5, Application US/10797393A
; Publication No. US20040219649A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Hans Sejr
; APPLICANT: Pedersen, Sven
; APPLICANT: Feestersen, Rikke Monica
; TITLE OF INVENTION: ALCOHOL PRODUCT PROCESSES
; FILE REFERENCE: 10391.200-US
; CURRENT APPLICATION NUMBER: US/10/797,393A
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-797-393A-5
Query Match 100.0%; Score 2684; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.7e-213;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGSSTTATCNADQKCYCG 60
Db 2 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGSSTTATCNADQKCYCG 61
Qy 61 TWQGIIDKLDYIQGMGFTAIWITPVAQLPQTAYGDAYHGYWQODIYSLNENYGTADDL 120
Db 62 TWQGIIDKLDYIQGMGFTAIWITPVAQLPQTAYGDAYHGYWQODIYSLNENYGTADDL 121
Qy 121 KALSALHERGMYLMDVVDVANHMGVDGAGSSVDYSVFKPFSQDYFHPFCFIQNYEDQTQ 180
Db 122 KALSALHERGMYLMDVVDVANHMGVDGAGSSVDYSVFKPFSQDYFHPFCFIQNYEDQTQ 181
Qy 181 VEDCWLGNVTSLPDLDTTKDVKVKNWYDWGSLVSNYSIDGLRIDTVKRVQKDFWPGYN 240
Db 182 VEDCWLGNVTSLPDLDTTKDVKVKNWYDWGSLVSNYSIDGLRIDTVKRVQKDFWPGYN 241
Qy 241 KAAGVYCI GEVLGDGPAYTCYQNVMDGVNLNPIYPLNAPKSTSGSMDDLNNINTVK 300
Db 242 KAAGVYCI GEVLGDGPAYTCYQNVMDGVNLNPIYPLNAPKSTSGSMDDLNNINTVK 301
Qy 301 SDPCDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGQSOHYAGGND 360
Db 302 SDPCDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGQSOHYAGGND 361
Qy 361 PANREATWLSGYPDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRGT 420
Db 362 PANREATWLSGYPDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRGT 421

[illegible]

RESULT 4
US-10-877-849-40

; Sequence 40, Application US/10877849
; Publication No. US20050054071A1

; GENERAL INFORMATION:

Query Match	Score	DB 17	Length
Best Local Similarity	100.0%	2684	608
Matches 498: Conservative	100.0%	Pred. No. 3.5e-213	
Matches 498: Conservative	0	Mismatches	0
Matches 498: Conservative	0	Indels	0
Matches 498: Conservative	0	Gaps	0

Qy	61	TWOGI	IIDLKLDY	IQMG	GFTAIW	ITPT	TAQLP	OTTAY	GD	YHGY	WOOD	IYSL	NENY	GTTADD	120
Db	61	TWOGI	IIDLKLDY	IQMG	GFTAIW	ITPT	TAQLP	OTTAY	GD	YHGY	WOOD	IYSL	NENY	GTTADD	120

	Qy	Db
181	VEDCWLGDNTVSLPDLDTTKDVVKNWEYDWVGSLSVSNYSIDGLRIDTDTVKEHVQKDFWPFGYN	240
181	VEDCWLGDNTVSLPDLDTTKDVVKNWEYDWVGSLSVSNYSIDGLRIDTDTVKEHVQKDFWPFGYN	240

	Qy	301	SDCPDSTLLGTFVENHDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGOEQHYAGGND	360
	Dy	301	SDCPDSTLLGTFVENHDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGOEQHYAGGND	360

Accession	Protein	Length
QY	QY	488
421	421	480
DG	DG	480

```
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connelly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; FILE REFERENCE: 10345-200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 18
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-18

Query Match          99.6%; Score 2674; DB 16; Length 499;
Best Local Similarity 99.6%; Pred. No. 1.8e-212;
Matches 496; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCYGG 60
DB 2 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCYGG 61
QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTQALPQTAYGDAYHGYWQODIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTQALPQTAYGDAYHGYWQODIYSLNENYGTADDL 121
QY 121 KALSSALHERGMYLMDVVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
DB 122 KALSSALHERGMYLMDVVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181
QY 181 VEDCWLGDNVTSPLDPTTKDVVKNEWYDWVGSLSVNSYSDGLRIDTVKHVKQDFWPGYN 240
DB 182 VEDCWLGDNVTSPLDPTTKDVVKNEWYDWVGSLSVNSYSDGLRIDTVKHVKQDFWPGYN 241
QY 241 KAAGYVCIGEVLGDGPATCTPQNVMDGVNLNPIYPIYLLNAPFKSTSGSMDDLNNMINTVK 300
DB 242 KAAGYVCIGEVLGDGPATCTPQNVMDGVNLNPIYPIYLLNAPFKSTSGSMDDLNNMINTVK 301
QY 301 SDPCDSTLLGTFFVENHNDNPFASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGND 360
DB 302 SDPCDSTLLGTFFVENHNDNPFASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGND 361
QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRGT 420
DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRGT 421
QY 421 DGSQIVTILSNKGASGDSYTLSSGAGYTAGOQLTEVIGCTTIVTSGDNVPVPMAGGLP 480
DB 422 DGSQIVTILSNKGASGDSYTLSSGAGYTAGOQLTEVIGCTTIVTSGDNVPVPMAGGLP 481
QY 481 RVLYPEKLAGSKICSS 498
DB 482 RVLYPEKLAGSKICSS 499

RESULT 7
US-10-815-495-22
; Sequence 22, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connelly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; FILE REFERENCE: 10345-200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.2
```

```
; SEQ ID NO 22
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-22

Query Match          99.2%; Score 2662; DB 16; Length 498;
Best Local Similarity 99.6%; Pred. No. 1.8e-211;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCYGG 60
DB 2 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCYGG 61
QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTQALPQTAYGDAYHGYWQODIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTQALPQTAYGDAYHGYWQODIYSLNENYGTADDL 121
QY 121 KALSSALHERGMYLMDVVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
DB 122 KALSSALHERGMYLMDVVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181
QY 181 VEDCWLGDNVTSPLDPTTKDVVKNEWYDWVGSLSVNSYSDGLRIDTVKHVKQDFWPGYN 240
DB 182 VEDCWLGDNVTSPLDPTTKDVVKNEWYDWVGSLSVNSYSDGLRIDTVKHVKQDFWPGYN 241
QY 241 KAAGYVCIGEVLGDGPATCTPQNVMDGVNLNPIYPIYLLNAPFKSTSGSMDDLNNMINTVK 300
DB 242 KAAGYVCIGEVLGDGPATCTPQNVMDGVNLNPIYPIYLLNAPFKSTSGSMDDLNNMINTVK 301
QY 301 SDPCDSTLLGTFFVENHNDNPFASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGND 360
DB 302 SDPCDSTLLGTFFVENHNDNPFASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGND 361
QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRGT 420
DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRGT 421
QY 421 DGSQIVTILSNKGASGDSYTLSSGAGYTAGOQLTEVIGCTTIVTSGDNVPVPMAGGLP 480
DB 422 DGSQIVTILSNKGASGDSYTLSSGAGYTAGOQLTEVIGCTTIVTSGDNVPVPMAGGLP 481
QY 481 RVLYPEKLAGSKIC 495
DB 482 RVLYPEKLAGSKIC 496

RESULT 8
US-10-184-771-10
; Sequence 10, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borcherdt, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-10-184-771-10

Query Match          95.8%; Score 2572; DB 14; Length 478;
Best Local Similarity 99.8%; Pred. No. 4.7e-204;
```

Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGTTCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 80
|||||
DB 1 ATPADWRSQSIYFLLTDRFARTDGTTCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 60
|||||

QY 81 WITPVTQALPQTTAYGDAYHGYWQDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 140
|||||
DB 61 WITPVTQALPQTTAYGDAYHGYWQDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 120
|||||

QY 141 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFQNTYEDQTVEDCWLGDNTVSLPDLDTTK 200
|||||
DB 121 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFQNTYEDQTVEDCWLGDNTVSLPDLDTTK 180
|||||

QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYVYICIGEVLDGDPAYTC 260
|||||
DB 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYVYICIGEVLDGDPAYTC 240
|||||

QY 261 PYQNVMDGVLNPIYYPLLNAPKSTSGMDDLNNMINTVKS DCPDSTLLGTTFVENHNDPR 320
|||||
DB 241 PYQNVMDGVLNPIYYPLLNAPKSTSGMDDLNNMINTVKS DCPDSTLLGTTFVENHNDPR 300
|||||

QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 380
|||||
DB 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 360
|||||

QY 381 LIASANAIRNYAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 440
|||||
DB 361 LIASANAIRNYAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 420
|||||

QY 441 LSLSGAGYTAGQQLTEVIGCTTGVTVGSDGNVPPVPMAGGLPRVLYPTEKLAGSKICSSS 498
|||||
DB 421 LSLSGAGYTAGQQLTEVIGCTTGVTVGSDGNVPPVPMAGGLPRVLYPTEKLAGSKICSSS 478
|||||

RESULT 9

US-10-186-042-7

; Sequence 7, Application US/10186042
; Publication No. US20030171236A1

GENERAL INFORMATION:

; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US

; CURRENT APPLICATION NUMBER: US/10/186,042

; PRIOR FILING DATE: 2002-06-28

; PRIOR APPLICATION NUMBER: US/09/672,459

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: 09/182,859

; PRIOR FILING DATE: 1998-10-29

; PRIOR APPLICATION NUMBER: 0515/96

; PRIOR FILING DATE: 1996-04-30

; PRIOR APPLICATION NUMBER: 0712/96

; PRIOR FILING DATE: 1996-06-28

; PRIOR APPLICATION NUMBER: 0775/96

; PRIOR FILING DATE: 1996-07-11

; PRIOR APPLICATION NUMBER: 1263/96

; PRIOR FILING DATE: 1996-11-08

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 478

; TYPE: PRT

; ORGANISM: Bacillus licheniformis

US-10-186-042-7

Query Match 95.8%; Score 2572; DB 14; Length 478;
Best Local Similarity 99.8%; Pred. No. 4.7e-204;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGTTCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 80
|||||

DB 1 ATPADWRSQSIYFLLTDRFARTDGTTCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 60
|||||

QY 81 WITPVTQALPQTTAYGDAYHGYWQDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 140
|||||

DB 61 WITPVTQALPQTTAYGDAYHGYWQDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 120
|||||

QY 141 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFQNTYEDQTVEDCWLGDNTVSLPDLDTTK 200
|||||

DB 121 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFQNTYEDQTVEDCWLGDNTVSLPDLDTTK 180
|||||

QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYVYICIGEVLDGDPAYTC 260
|||||

DB 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYVYICIGEVLDGDPAYTC 240
|||||

QY 261 PYQNVMDGVLNPIYYPLLNAPKSTSGMDDLNNMINTVKS DCPDSTLLGTTFVENHNDPR 320
|||||

DB 241 PYQNVMDGVLNPIYYPLLNAPKSTSGMDDLNNMINTVKS DCPDSTLLGTTFVENHNDPR 300
|||||

QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 380
|||||

DB 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 360
|||||

QY 381 LIASANAIRNYAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 440
|||||

DB 361 LIASANAIRNYAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 420
|||||

QY 441 LSLSGAGYTAGQQLTEVIGCTTGVTVGSDGNVPPVPMAGGLPRVLYPTEKLAGSKICSSS 498
|||||

DB 421 LSLSGAGYTAGQQLTEVIGCTTGVTVGSDGNVPPVPMAGGLPRVLYPTEKLAGSKICSSS 478
|||||

RESULT 10

US-10-644-187-7

; Sequence 7, Application US/10644187

; Publication No. US20040048351A1

GENERAL INFORMATION:

; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US

; CURRENT APPLICATION NUMBER: US/10/644,187

; CURRENT FILING DATE: 2003-08-20

; PRIOR APPLICATION NUMBER: 09/182,859

; PRIOR FILING DATE: 1998-10-29

; PRIOR APPLICATION NUMBER: 0515/96

; PRIOR FILING DATE: 1996-04-30

; PRIOR APPLICATION NUMBER: 0712/96

; PRIOR FILING DATE: 1996-06-28

; PRIOR APPLICATION NUMBER: 0775/96

; PRIOR FILING DATE: 1996-07-11

; PRIOR APPLICATION NUMBER: 1263/96

; PRIOR FILING DATE: 1996-11-08

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 478

; TYPE: PRT

; ORGANISM: Bacillus licheniformis

US-10-644-187-7

Query Match 95.8%; Score 2572; DB 15; Length 478;
Best Local Similarity 99.8%; Pred. No. 4.7e-204;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGTTCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 80
|||||

DB 1 ATPADWRSQSIYFLLTDRFARTDGTTCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 60
|||||

QY 81 WITPVTQALPQTTAYGDAYHGYWQDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 140
|||||

DB 61 WITPVTQALPQTTAYGDAYHGYWQDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 120
|||||

```
QY 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIONYEDQTOVEDCWLGDNTVSLPDLDTTK 200
DB 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIONYEDQTOVEDCWLGDNTVSLPDLDTTK 180
QY 201 DVVKNEWDMVGSLSVNSYSIDGLRIDTVKHVKQDFWPGYNKAAGYVCIGEVLDGDPAYTC 260
DB 181 DVVKNEWDMVGSLSVNSYSIDGLRIDTVKHVKQDFWPGYNKAAGYVCIGEVLDGDPAYTC 240
QY 261 PYQVMDGVLNYPYIYPLLNAPKSTSGMDDLNNMINTVKSDDPDLTLLGTFVENHNDNPR 320
DB 241 PYQVMDGVLNYPYIYPLLNAPKSTSGMDDLNNMINTVKSDDPDLTLLGTFVENHNDNPR 300
QY 321 FASYTNDIALAKNVAFAFIILNDGIPYIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 380
DB 301 FASYTNDIALAKNVAFAFIILNDGIPYIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNVAISKDTGFTYKNWPIYKDDTTIAMRKGTGDSQIIVTILSNKGASGDSYT 440
DB 361 LIASANAIRNVAISKDTGFTYKNWPIYKDDTTIAMRKGTGDSQIIVTILSNKGASGDSYT 420
QY 441 LSLSGAGYTAGOOLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLVYPTTEKLAGSKICSSS 498
DB 421 LSLSGAGYTAGOOLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLVYPTTEKLAGSKICSSS 478
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RESULT 11

```
US-10-926-720-10
; Sequence 10, Application US/10926720
; Publication No. US20050019886A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; Bisgard-Frantzen, Henrik
; Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/926,720
; FILING DATE: 26-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10
```

```
Query Match 95.8%; Score 2572; DB 17; Length 478;
Best Local Similarity 99.8%; Pred. No. 4.7e-204;
```

```
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 ATPADWRSQSIYFLLTORFARTDGTATCATADOKYCGGTWQGIIDKLDYIQMGFTAI 80
DB 1 ATPADWRSQSIYFLLTORFARTDGTATCATADOKYCGGTWQGIIDKLDYIQMGFTAI 60
QY 81 WITPVTQALPQTAYGDAYHGYWQODIYSLNENYGTADDLKAALSSALHERGMWLMVDVVA 140
DB 61 WITPVTQALPQTAYGDAYHGYWQODIYSLNENYGTADDLKAALSSALHERGMWLMVDVVA 120
QY 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIONYEDQTOVEDCWLGDNTVSLPDLDTTK 200
DB 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIONYEDQTOVEDCWLGDNTVSLPDLDTTK 180
QY 201 DVVKNEWDMVGSLSVNSYSIDGLRIDTVKHVKQDFWPGYNKAAGYVCIGEVLDGDPAYTC 260
DB 181 DVVKNEWDMVGSLSVNSYSIDGLRIDTVKHVKQDFWPGYNKAAGYVCIGEVLDGDPAYTC 240
QY 261 PYQVMDGVLNYPYIYPLLNAPKSTSGMDDLNNMINTVKSDDPDLTLLGTFVENHNDNPR 320
DB 241 PYQVMDGVLNYPYIYPLLNAPKSTSGMDDLNNMINTVKSDDPDLTLLGTFVENHNDNPR 300
QY 321 FASYTNDIALAKNVAFAFIILNDGIPYIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 380
DB 301 FASYTNDIALAKNVAFAFIILNDGIPYIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNVAISKDTGFTYKNWPIYKDDTTIAMRKGTGDSQIIVTILSNKGASGDSYT 440
DB 361 LIASANAIRNVAISKDTGFTYKNWPIYKDDTTIAMRKGTGDSQIIVTILSNKGASGDSYT 420
QY 441 LSLSGAGYTAGOOLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLVYPTTEKLAGSKICSSS 498
DB 421 LSLSGAGYTAGOOLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLVYPTTEKLAGSKICSSS 478
```

RESULT 12

```
US-10-980-759-7
; Sequence 7, Application US/10980759
; Publication No. US20050118695A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/980,759
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-980-759-7
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Query Match 95.8%; Score 2572; DB 17; Length 478;
Best Local Similarity 99.8%; Pred. No. 4.7e-204;
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Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 ATPADWRSQSIYFLLTORFARTDGTATCATADOKYCGGTWQGIIDKLDYIQMGFTAI 80
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Db 1 ATPADWRSQSIYFLLTDRPARTDGGTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 140
Db 61 WITPVTAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 120
QY 141 NHMGYDGAGSSVDYSVFPPSSQDYFHPFCFQNYEDQTVEDCWLGDNTVSLPDLDTTK 200
Db 121 NHMGYDGAGSSVDYSVFPPSSQDYFHPFCFQNYEDQTVEDCWLGDNTVSLPDLDTTK 180
QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYVICGEVLDDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYVICGEVLDDGDPAYTC 240
QY 261 PYQNVMDGVLNPIIYYPPLNAPKSTSGMDDLYNMINTVKSDCPDSTLLGTGFVENHDNPR 320
Db 241 PYQNVMDGVLNPIIYYPPLNAPKSTSGMDDLYNMINTVKSDCPDSTLLGTGFVENHDNPR 300
QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 440
Db 361 LIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 420
QY 441 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
Db 421 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVVPVPMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 13

US-11-064-196-10
; Sequence 10, Application US/11064196
; Publication No. US20050170487A1
; GENERAL INFORMATION:

; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/11/064,196
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10

; LENGTH: 478

; TYPE: PR

; ORGANISM: A. oryzae

US-11-064-196-10

Query Match 95.8%; Score 2572; DB 20; Length 478;
Best Local Similarity 99.8%; Pred. No. 4.7e-204;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRPARTDGGTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRPARTDGGTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 140
Db 61 WITPVTAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 120
QY 141 NHMGYDGAGSSVDYSVFPPSSQDYFHPFCFQNYEDQTVEDCWLGDNTVSLPDLDTTK 200
Db 121 NHMGYDGAGSSVDYSVFPPSSQDYFHPFCFQNYEDQTVEDCWLGDNTVSLPDLDTTK 180
QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYVICGEVLDDGDPAYTC 260

Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYVICGEVLDDGDPAYTC 240
QY 261 PYQNVMDGVLNPIIYYPPLNAPKSTSGMDDLYNMINTVKSDCPDSTLLGTGFVENHDNPR 320
Db 241 PYQNVMDGVLNPIIYYPPLNAPKSTSGMDDLYNMINTVKSDCPDSTLLGTGFVENHDNPR 300
QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 440
Db 361 LIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 420
QY 441 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
Db 421 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVVPVPMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 14

US-10-877-849-43

; Sequence 43, Application US/10877849

; Publication No. US20050054071A1

; GENERAL INFORMATION:

; APPLICANT: Udagawa, Hiroaki

; APPLICANT: Taira, Rikako

; APPLICANT: Tkagi, Shinobu

; APPLICANT: Allain, Eric

; APPLICANT: Hjort, Carsten

; APPLICANT: Vikso-Nielsen, Anders

; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING

; FILE REFERENCE: 10490.500-US

; CURRENT APPLICATION NUMBER: US/10/877,849

; CURRENT FILING DATE: 2004-06-25

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 43

; LENGTH: 476

; TYPE: PR

; ORGANISM: Aspergillus oryzae

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: (1)..(476)

US-10-877-849-43

Query Match 95.8%; Score 2570; DB 17; Length 476;

Best Local Similarity 100.0%; Pred. No. 6.9e-204;

Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRPARTDGGTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRPARTDGGTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 140
Db 61 WITPVTAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 120
QY 141 NHMGYDGAGSSVDYSVFPPSSQDYFHPFCFQNYEDQTVEDCWLGDNTVSLPDLDTTK 200
Db 121 NHMGYDGAGSSVDYSVFPPSSQDYFHPFCFQNYEDQTVEDCWLGDNTVSLPDLDTTK 180
QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYVICGEVLDDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYVICGEVLDDGDPAYTC 240
QY 261 PYQNVMDGVLNPIIYYPPLNAPKSTSGMDDLYNMINTVKSDCPDSTLLGTGFVENHDNPR 320
Db 241 PYQNVMDGVLNPIIYYPPLNAPKSTSGMDDLYNMINTVKSDCPDSTLLGTGFVENHDNPR 300
QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 360

Qy	381	LTASANAIRNYAISKDTGFTVKNWPIYKDDTTAMRKGTGDSQIVILSNKSGASGSYTT	440
Db	361	LTASANAIRNYAISKDTGFTVKNWPIYKDDTTAMRKGTGDSQIVILSNKSGASGSYTT	420
Qy	441	LSLSGAGYTAGQQLTEVIGCTTTVTSGDGNVPVMAGGLPRVLYPTKLAGSKICS	496
Db	421	LSLSGAGYTAGQQLTEVIGCTTTVTSGDGNVPVMAGGLPRVLYPTKLAGSKICS	476

```

RESULT 15
US-10-228-063-45
; Sequence 45, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lanahan, Mike
; TITLE OF INVENTION: Self-processing Plants and Plant Parts
; FILE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1095
; TYPE: prt
; ORGANISM: Aspergillus shiirousami
US-10-228-063-45

```

Query Match.	95.7%;	Score 2569;	DB 14;	Length 1095;						
Best Local Similarity	99.8%;	Pred. No.2.7e-203;								
Matches 477;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;						
Qy	21	ATPADWSQSIFYLLTDRFARTDGS	TATCN	TADQKYCGGTWOGI	IIDKLDVIQGMGF	TAI 80				
Db	1	ATPADWSQSIFYLLTDRFARTDGS	TATCN	TADQKYCGGTWOGI	IIDKLDVIQGMGF	TAI 60				
Qy	81	WITPVTAQLPOTTAIGDAYHGYYOOD	YISL	NENYGTADDL	KALSALHGERGMYL	MVDVVA 140				
Db	61	WITPVTAQLPOTTAIGDAYHGYYOOD	YISL	NENYGTADDL	KALSALHGERGMYL	MVDVVA 120				
Qy	141	NHMGYDAGAGSSVDYSVFKPSSQDY	FHPFCFI	QNYVEDQ	TQVEDCWL	GBNTVTSLPDLD	DTTK 200			
Db	121	NHMGYDAGAGSSVDYSVFKPSSQDY	FHPFCFI	QNYVEDQ	TQVEDCWL	GBNTVTSLPDLD	DTTK 180			
Qy	201	DVVKNEWYDWVGSIVUSNYSIDGL	RIDT	VKHVQKD	FWPGYNKAA	GYCIGEVL	DGD	PAYTC 260		
Db	181	DVVKNEWYDWVGSIVUSNYSIDGL	RIDT	VKHVQKD	FWPGYNKAA	GYCIGEVL	D	VPAYTC 240		
Qy	261	PYQNMVGVLNYPITYPLLN	AFKSTSGS	MDLLYN	MINITVKS	DCDPD	STLLGTFV	ENHDN	PNR 320	
Db	241	PYQNMVGVLNYPITYPLLN	AFKSTSGS	MDLLYN	MINITVKS	DCDPD	STLLGTFV	ENHDN	PNR 300	
Qy	321	FASYTNDIALAKNVAAFI	ILNDG	PIIYAG	QEQHYAG	GNDPAN	REATW	LSGYPT	DS	ELYK 380
Db	301	FASYTNDIALAKNVAAFI	ILNDG	PIIYAG	QEQHYAG	GNDPAN	REATW	LSGYPT	DS	ELYK 360
Qy	381	LIASANAIRNYAISKDTGF	VTKWPIY	KDPTTT	AMRKG	TDPGSQ	IVTIL	SNK	AGS	SDSYT 440
Db	361	LIASANAIRNYAISKDTGF	VTKWPIY	KDPTTT	AMRKG	TDPGSQ	IVTIL	SNK	AGS	SDSYT 420
Qy	441	LSLSGAGYTAGQQLTE	VGICTT	VTVSD	GNVPVPM	AGGL	PRVLYP	TEK	LAGS	KICSSS 498
Db	421	LSLSGAGYTAGQQLTE	VGICTT	VTVSD	GNVPVPM	AGGL	PRVLYP	TEK	LAGS	KICSSS 478

Search completed: November 7, 2005, 18:45:02
Job time : 274.151 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2005, 18:40:32 ; Search time 1.50579 Seconds
(without alignments)
830.671 Million cell updates/sec

Title: US-10-820-200-2 COPY 98 110

Perfect score: 78

Sequence: 1 AYHGYWQQDIYSL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79: *

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1: pir1:*
```

2: p1r2:★

3: pir3:★

4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query \$			DB	ID	Description
		Match	Length				
1	78	100.0	498	2	A48305	alpha-amylase [EC	
2	78	100.0	499	1	ALAS1	alpha-amylase [EC	
3	78	100.0	499	1	ALAS3	alpha-amylase [EC	
4	78	100.0	499	2	JS0663	alpha-amylase [EC	
5	78	100.0	499	2	JT0466	alpha-amylase [EC	
6	78	100.0	499	2	JN0588	alpha-amylase [EC	
7	78	100.0	499	2	B40305	alpha-amylase [EC	
8	67	85.9	513	2	T38770	alpha-amylase a p	
9	66	84.6	631	2	S72287	alpha-amylase [EC	
10	64	82.1	484	1	A35282	alpha-amylase [EC	
11	64	82.1	507	2	S33921	alpha-amylase [EC	
12	62	62.1	507	2	JK0201	alpha-amylase [EC	
13	62	79.5	478	2	JC4510	pullulanase [EC 3	
14	59	75.6	624	1	T31478	alpha-amylase [EC	
15	58	74.4	494	1	ALBYAF	alpha-amylase [EC	
16	56	71.8	478	2	T40860	probable alpha-am	
17	54	69.2	491	2	T38448	probable alpha-am	
18	53	67.9	564	2	T41503	alpha-amylase - f	
19	52	66.7	581	2	S62505	probable alpha-am	
20	50	64.1	512	2	S23355	alpha-amylase [EC	
21	50	64.1	512	2	S06115	alpha-amylase [EC	
22	50	64.1	625	2	T41603	alpha-amylase - f	
23	49	62.8	528	1	ALBSK	alpha-amylase [EC	
24	49	62.8	690	2	B82409	alpha-amylase VCA	
25	49	62.8	712	1	ALBSG3	cyclomaltodextrin	
26	49	62.8	713	1	ALBSG7	cyclomaltodextrin	
27	49	62.8	713	1	ALBSG1	cyclomaltodextrin	
28	49	62.8	713	1	ALBSR	cyclomaltodextrin	
29	49	62.8	713	2	A58900	cyclomaltodextrin	

ALIGNMENTS

RESULT 1

A48305
alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori
C/Spectes: Aspergillus awamori
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
C/Accession: A48305
R/Korman, D.R.; Bayliss, P.T.; Barnett, C.C.; Carmona, C.L.; Koo
Curr. Genet. 17, 203-212, 1990
A/Title: Cloning, characterization, and expression of two alpha
A/Reference number: A48305; MUID:90254827; PMID:2340591
A/Accession: A48305
A/Status: preliminary; not compared with conceptual translation

Query Match 100.0%; Score 78; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13: Conservative 0; Mismatches 0; Indels

Qy 1 AYHGYWQDIYSL 13
|||
db 99 AYHGYWOODIYSL 111

RESULT 2

ALAS1
 Alpha-amylase (EC 3.2.1.1) 1 precursor [validated] - Aspergillus oryzae
 N; Alternate names: alpha-amylase isozyme II; glycogenase; Taka-amylase A
 C; Species: Aspergillus oryzae
 C; Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
 C; Accession: S04548; A33214; J50240; A91930; A93767; A10627
 R; Wiersel, S.; Lachmund, A.; Wildhardt, G.; Rutkowski, E.
 Mol. Microbiol. 3, 3-14, 1989
 A; Rittle: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon
 A; Reference number: S04548; MUID:89237897; PMID:2785629

Gene 79, 107-117, 1989
A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing
A;Reference number: JS0240; MUID:89378767; PMID:2789162
A;Accession: JS0240
A;Molecule type: DNA
A;Residues: 1-499 <GEN>
A;Genetics: AMY2
A;Note: the authors refer to this as isozyme II
R;Isemura, S.; Ikenaka, T.
J. Biochem. 74, 1-10, 1973
A;Reference number: A91930; MUID:74001521; PMID:4733850
A;Accession: A91930
A;Molecule type: protein
A;Residues: 206-225 <ISE>
R;Narita, K.
Proc. Jpn. Acad. 51, 285-290, 1975
A;Reference number: A93767
A;Accession: A93767
A;Molecule type: protein
A;Residues: 434-443, 446-447, 'Q', 449-458, 'GTTV', 459-464, 467-468, 'B', 470, 'B', 472-499 <NAR>
R;Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
A;Title: Structure and possible catalytic residues of Taka-amylase A.
A;Reference number: A37454; MUID:84212370; PMID:6609921
A;Contents: annotation; X-ray crystallography, 3.0 angstroms
submitted to the Brookhaven Protein Data Bank, August 1992
A;Reference number: A51548; PDB:6TAA
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 22-497
C;Comment: One atom of calcium per molecule is essential for activity.
C;Genetics: <AMY1>
A;Gene: amy1
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Genetics: <AMY2>
A;Gene: amy2; AmyII
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; polys
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase 1 #status experimental <MAT>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
F;142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;227,251,318/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 78; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDIYSL 13
|||||
Db 99 AYHGYYQDIYSL 111

RESULT 3
ALAS3
alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae
N;Alternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S04549; A33215; A44713
R;Wiesel, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon c
A;Reference number: S04548; MUID:89237897; PMID:2785629
A;Accession: S04549
A;Molecule type: DNA
A;Residues: 1-499 <WIR>
A;Cross-references: UNIPROT:Q96TH4; EMBL:X12727; NID:G2454; PIDN:CAA31220.1; PID:G295923

A;Accession: A33215
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-499 <WIR>
A;Cross-references: GB:X12727; NID:G2454; PIDN:CAA31220.1; PID:G295922
R;Genes, M.J.; Dove, M.J.; Seligy, V.L.
Gene 79, 107-117, 1989
A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containin
A;Reference number: JS0240; MUID:89378767; PMID:2789162
A;Accession: A44713
A;Molecule type: DNA
A;Residues: 1-499 <GEN>
A;Note: the authors refer to this as isozyme I
R;Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
A;Title: Structure and possible catalytic residues of Taka-amylase A.
A;Reference number: A37454; MUID:84212370; PMID:6609921
A;Contents: annotation; X-ray crystallography, 3.0 angstroms
C;Comment: One atom of calcium per molecule is essential for activity.
C;Genetics:
A;Gene: amy3; AmyI
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; meta
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase 3 #status experimental <MAT>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
F;142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;231,251,318/Active site: His, Glu, Asp #status experimental

Query Match 100.0%; Score 78; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDIYSL 13
|||||
Db 99 AYHGYYQDIYSL 111

RESULT 4
JS0663
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus sp.
C;Species: Aspergillus sp.
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
C;Accession: JS0663
R;Shibuya, I.; Tamura, G.; Ishikawa, T.; Hara, S.
Biosci. Biotechnol. Biochem. 56, 174-179, 1992
A;Title: Cloning of the alpha-amylase cDNA of Aspergillus shirousami and its expressio
A;Reference number: JS0663; MUID:92323146; PMID:1368777
A;Accession: JS0663
A;Molecule type: mRNA
A;Residues: 1-499 <SHI>
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase #status predicted <ALP>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDIYSL 13
|||||

Db 99 AYHGYWQDIYSL 111

RESULT 5
JT0466
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N/Alternate names: glycogenase; Taka-amylase A
C/Species: Aspergillus oryzae
C/Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C/Accession: JT0466
R/Tada, S.; Iimura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.
Agric. Biol. Chem. 53, 593-599, 1989
A/Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergillus oryzae
A/Reference number: JT0466
A/Accession: JT0466
A/Molecule type: DNA
A/Residues: 1-499 <TAD>
A/Cross-references: UNIPROT:P10529
C/Comment: See also PIR:JK0201 and PIR:JS0240.
C/Comment: One atom of calcium per molecule is essential for activity.
C/Genetics:
A/Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C/Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F/1-21/Domain: signal sequence #status predicted <SIG>
F/22-499/Product: alpha-amylase #status predicted <MAT>
F/194-321/Domain: alpha-amylase core homology <AMY>
F/218/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/231,251,318/Active site: His, Glu, Asp #status predicted

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
Db 99 AYHGYWQDIYSL 111

RESULT 6
JN0588
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N/Alternate names: Taka-amylase A
C/Species: Aspergillus oryzae
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: JN0588
R/Tsukagoshi, N.; Furukawa, M.; Nagaba, H.; Kiritu, N.; Tsuboi, A.; Udaoka, S.
Gene 84, 319-327, 1989
A/Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for multiple forms of the enzyme
A/Reference number: JN0588; MUID:90128276; PMID:2612911
A/Accession: JN0588
A/Molecule type: mRNA
A/Residues: 1-499 <TSU>
A/Cross-references: UNIPROT:Q96TH4
C/Comment: The alpha amylases are encoded by multigene family.
C/Genetics:
A/Gene: Taa-G1
A/Introns: 56/1; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C/Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F/1-21/Domain: signal sequence #status predicted <SIG>
F/22-499/Product: alpha-amylase #status predicted <MAT>
F/194-321/Domain: alpha-amylase core homology <AMY>
F/218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
Db 99 AYHGYWQDIYSL 111

RESULT 8
T38770
alpha-amylase a precursor - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T38770
R/Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A/Reference number: Z21751
A/Accession: T38770
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-513 <SKE>
A/Cross-references: UNIPROT:O14154; EMBL:Z98762; PIDN:CAB11471.1; GSPDB:GN00066; SPDB:S72270
A/Experimental source: strain 972h-; cosmid c4A8
C/Genetics:
A/Gene: SPDB:SPAC4A8.01
A/Map position: 1
C/Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

Query Match 85.9%; Score 67; DB 2; Length 513;
Best Local Similarity 76.9%; Pred. No. 0.0027;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
Db 100 AYHGYWQDIYSL 112

RESULT 9
S72270
alpha-amylase (EC 3.2.1.1) precursor - Cryptococcus sp. (strain CS2)
C/Species: Cryptococcus sp.
A/Variety: strain CS2
C/Date: 23-Apr-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
Db 99 AYHGYWQDIYSL 111

RESULT 7

B48305

alpha-amylase (EC 3.2.1.1) B precursor - Aspergillus awamori

C/Species: Aspergillus awamori

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C/Accession: B48305

R/Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.

Curr. Genet. 17, 203-212, 1990

A/Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspergillus awamori

A/Reference number: A48305; MUID:90254827; PMID:2340591

A/Accession: B48305

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-499 <KOR>

A/Cross-references: UNIPROT:Q02906

C/Function:

A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A/Pathway: glycogen/starch degradation

C/Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C/Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F/194-321/Domain: alpha-amylase core homology <AMY>

Query Match 100.0%; Score 78; DB 2; Length 499;

Best Local Similarity 100.0%; Pred. No. 4.1e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13

Db 99 AYHGYWQDIYSL 111

C;Accession: S72270
R;Iefuji, H.; Chino, M.; Kato, M.; Iimura, Y.
Biochem. J. 318, 989-996, 1996
A;Title: Raw-starch-digesting and thermostable alpha-amylase from the yeast *Cryptococcus*
A;Reference number: S72270; MUID:964333120; PMID:8836148
A;Accession: S72270
A;Molecule type: DNA
A;Residues: 1-631 <IEF>
A;Cross-references: UNIPROT:Q92394; EMBL:D83540; NID:g1595852; PIDN:BAA12010.1; PID:g159
A;Experimental source: strain S-2
C;Genetics:
A;Gene: amy-C82
A;Introns: 289/2; 326/2
C;Function:
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-631/Product: alpha-amylase #status predicted <MAT>
F;206-335/Domain: alpha-amylase core homology <AMY>
Query Match 84.6%; Score 66; DB 2; Length 631;
Best Local Similarity 76.9%; Pred. No. 0.005; Mismatches 1; Indels 2; Gaps 0;
Matches 10; Conservative 1; Mismatches 0; Gaps 0;
QY 1 AYHGYWQDIYSL 13
DB 105 AYHGYWQDIYEI 117
RESULT 10
A35282
alpha-amylase (EC 3.2.1.1) - *Aspergillus niger*
C;Species: *Aspergillus niger*
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A35282
R;Boel, E.; Brady, L.; Brzozowski, A.M.; Derewenda, Z.; Dodson, G.G.; Jensen, V.J.; Peter
Biochemistry 29, 6244-6249, 1990
A;Title: Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-angstrom
A;Reference number: A35282; MUID:91002514; PMID:2207069
A;Accession: A35282
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-484 <BOE>
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;173-300/Domain: alpha-amylase core homology <AMY>
Query Match 82.1%; Score 64; DB 1; Length 484;
Best Local Similarity 76.9%; Pred. No. 0.008; Mismatches 1; Indels 2; Gaps 0;
Matches 10; Conservative 1; Mismatches 0; Gaps 0;
QY 1 AYHGYWQDIYSL 13
DB 78 AYHGYWQDIYDV 90
RESULT 11
S33921
alpha-amylase (EC 3.2.1.1) SWA2 precursor - yeast (*Schwanniomyces occidentalis*)
N;Alternate names: alpha-1,4 glucanohydrolase
C;Species: *Schwanniomyces occidentalis*
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S33921
R;Claros, M.G.; Abarca, D.; Fernandez-Lobato, M.; Jimenez, A.
Curr. Genet. 24, 75-83, 1993
A;Title: Molecular structure of the SWA2 gene encoding an AMY1-related alpha-amylase fro
A;Reference number: S33921; MUID:93365041; PMID:8358835
A;Accession: S33921
A;Molecule type: DNA

A;Residues: 1-507 <CLA>
A;Cross-references: UNIPROT:Q08806; EMBL:X73497; NID:g396561; PIDN:CAA51912.1; PID:g3965
C;Genetics:
A;Gene: SWA2
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-507/Product: alpha-amylase #status predicted <MAT>
F;205-332/Domain: alpha-amylase core homology <AMY>
F;134,229/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 82.1%; Score 64; DB 2; Length 507;
Best Local Similarity 69.2%; Pred. No. 0.0084; Mismatches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 AYHGYWQDIYSL 13
DB 110 AYHGYWQDIYAI 122
RESULT 12
JK0201
alpha-amylase (EC 3.2.1.1) - *Aspergillus oryzae*
N;Alternate names: glycogenase; Taka-amylase A
C;Species: *Aspergillus oryzae*
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: JK0201
R;Toda, H.; Kondo, K.; Narita, K.
Proc. Jpn. Acad. 58B, 208-212, 1982
A;Title: The complete amino acid sequence of Taka-amylase A.
A;Reference number: JK0201
A;Accession: JK0201
A;Molecule type: protein
A;Residues: 1-478 <TOD>
A;Cross-references: UNIPROT:P10529
C;Comment: One atom of calcium per molecule is essential for the activity.
C;Comment: This enzyme is a glycoprotein.
C;Comment: See also PIR:JT0466 and PIR:JS0240.
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;173-300/Domain: alpha-amylase core homology <AMY>
F;197/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;210,230,297/Active site: His, Glu, Asp #status experimental
Query Match 79.5%; Score 62; DB 2; Length 478;
Best Local Similarity 84.6%; Pred. No. 0.017; Mismatches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AYHGYWQDIYSL 13
DB 78 AYHGYWQDIYSL 90
RESULT 13
JC4510
pullulanase (EC 3.2.1.41) precursor - yeast (*Lipomyces kononenkoae*)
N;Alternate names: LKAI protein; raw starch-degrading amylase
N;Contains: alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)
C;Species: *Lipomyces kononenkoae*
C;Date: 07-Feb-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
C;Accession: JC4510; PC4116
R;Steyn, A.J.C.; Marmur, J.; Pretorius, I.S.
Gene 166, 65-71, 1995
A;Title: Cloning, sequence analysis and expression in yeasts of a cDNA containing a Lip
A;Reference number: JC4510; MUID:96105202; PMID:8529895
A;Accession: JC4510
A;Molecule type: mRNA

A;Residues: 1-624 <STE>
A;Cross-references: UNIPROT:Q01117; GB:U30376; NID:g1173536; PIDN:AAC49622.1; PID:g11735
A;Experimental source: strain IGC4052B
A;Accession: PC4116
A;Molecule type: protein
A;Residues: 29-44 <ST2>
A;Experimental source: IGC4052B
C;Genetics:
A;Gene: LKAI
C;Function:
A;Description: hydrolyzes raw starch, degrading both alpha-1,4 and alpha-1,6 linkages
A;Pathway: glycogen/starch degradation
C;Superfamily: Lipomyces alpha-amylase; alpha-amylase core homology; glucoamylase starch
C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-624/Product: alpha-amylase #status predicted <MAT>
F;48-141/Domain: glucoamylase starch-binding domain homology <SBD>
F;320-447/Domain: alpha-amylase core homology <AMY>
F;177-185,297-311,387-430,587-622/Disulfide bonds: #status predicted
F;304,344/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;357,377,444/Active site: His, Glu, Asp #status predicted

Query Match 79.5%; Score 62; DB 1; Length 624;
Best Local Similarity 69.2%; Pred. No. 0.022;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
||||| :|||
Db 225 AYHGYWKMDFAL 237

RESULT 14
S31478
alpha-amylase (EC 3.2.1.1) - Thermoactinomyces vulgaris
C;Species: Thermoactinomyces vulgaris
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S31478
R;Hofemeister, B.; Koenig, S.; Hoang, V.; Engel, J.; Mayer, G.; Heese, O.; Hansen, G.; H
submitted to the EMBL Data Library, December 1992
A;Description: The gene amyTV coding for a non-glucogenic alpha-amylase from Thermoactin
A;Reference number: S31478
A;Accession: S31478
A;Molecule type: DNA
A;Residues: 1-482 <HOF>
A;Cross-references: UNIPROT:Q60051; EMBL:X69807; NID:g48289; PIDN:CAA49465.1; PID:g48290
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;194-319/Domain: alpha-amylase core homology <AMY>

Query Match 75.6%; Score 59; DB 2; Length 482;
Best Local Similarity 69.2%; Pred. No. 0.053;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
||||| :|||
Db 107 AYHGYWTFYSV 119

RESULT 15
ALBYAF
alpha-amylase (EC 3.2.1.1) precursor - yeast (Saccharomycopsis fibuligera)
C;Species: Saccharomycopsis fibuligera
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: S00064
R;Itoh, T.; Yamashita, I.; Fukui, S.
FEBS Lett. 219, 339-342, 1987
A;Title: Nucleotide sequence of the alpha-amylase gene (ALP1) in the yeast Saccharomycop
A;Reference number: S00064; MUID:87276512; PMID:3497057
A;Accession: S00064
A;Molecule type: DNA

A;Residues: 1-494 <ITO>
A;Cross-references: UNIPROT:P21567; EMBL:X05791; NID:g4847; PIDN:CAA29233.1; PID:g4848
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in having 368-Th
C;Genetics:
A;Gene: ALP1
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: calcium; extracellular protein; glycoprotein; glycosidase; hydrolase; metal
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-494/Product: alpha-amylase #status predicted <MAT>
F;200-327/Domain: alpha-amylase core homology <AMY>
F;57-65,177-191,267-310,462-493/Disulfide bonds: #status predicted
F;148,189,202,237/Binding site: calcium (Asn, Gln, Asp, His) #status predicted
F;224/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;233,257,324/Active site: Asp, Glu, Asp #status predicted

Query Match 74.4%; Score 58; DB 1; Length 494;
Best Local Similarity 61.5%; Pred. No. 0.079;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
||||| :|||
Db 105 AYHGYWKNYKI 117

Search completed: November 7, 2005, 18:58:45
Job time : 1.50579 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:24:00 ; Search time 6.97683 Seconds
(without alignments)
954.162 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110
Perfect score: 78
Sequence: 1 AYHGWQDIYSL 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	100.0	498	1 AMYA ASPAW	Q02905 aspergillus
2	78	100.0	498	2 Q76CT3	Q76ct3 aspergillus
3	78	100.0	499	1 AMYA ASPOR	P10529 aspergillus
4	78	100.0	499	1 AMYA ASPAW	Q02906 aspergillus
5	78	100.0	499	1 AMY ASPSH	P30292 aspergillus
6	78	100.0	499	2 Q96TH4	Q96th4 aspergillus
7	78	100.0	499	2 Q76L39	Q76l39 aspergillus
8	78	100.0	499	2 Q7LV45	Q7lv45 aspergillus
9	75	96.2	490	2 Q9UV07	Q9uv07 emericeila
10	68	87.2	128	2 O15751	O15751 dictyosteli
11	67	85.9	513	1 AMY3 SCHPO	O14154 schizosacch
12	66	84.6	631	2 Q92354	Q92394 cryptococcu
13	64	82.1	484	1 AMYA ASPNG	P56271 aspergillus
14	64	82.1	507	1 AMY2 DEBEC	Q08806 debaryomyce
15	64	82.1	634	2 Q76L36	Q76l36 aspergillus
16	63	80.8	640	2 O13296	O13296 aspergillus
17	62	79.5	624	1 AMY1 LIPKO	Q01117 lipomyces k
18	62	79.5	647	2 Q6YF33	Q6yf33 lipomyces s
19	59	75.6	482	2 Q60051	Q60051 thermocactin
20	59	75.6	492	2 Q7SDU6	Q7sdj6 neurospora
21	58	74.4	494	1 AMY1 SAGFI	P21567 saccharomyc
22	56	71.8	478	1 YQ29 SCHPO	O10427 schizosacch
23	54	69.2	491	2 O13956	O13996 schizosacch
24	54	69.2	623	2 Q9UV09	Q9uv09 emericeila
25	53	67.9	564	1 AMY4 SCHPO	Q9y789 schizosacch
26	52	66.7	533	2 Q7S4X0	Q7s4k0 neurospora
27	52	66.7	581	1 AMY1 SCHPO	Q09840 schizosacch
28	52	66.7	711	2 Q992E3	Q992b3 streptococc
29	50	64.1	499	2 Q8J1B4	Q8j1e4 lipomyces k
30	50	64.1	512	1 AMY1 DEBEC	P19289 debaryomyce
31	50	64.1	625	2 O74922	O74922 schizosacch

32	49	62.8	528	1	AMY_BACCI	P08137 bacillus ci
33	49	62.8	686	2	Q87FR2	Q87fr2 vibrio para
34	49	62.8	687	2	Q7MCL0	Q7mcl0 vibrio vuln
35	49	62.8	687	2	Q8D5L1	Q8d5l1 vibrio vuln
36	49	62.8	690	2	Q9KL86	Q9kl86 vibrio chol
37	49	62.8	712	1	CDGT_BACS3	P09121 bacillus sp
38	49	62.8	712	2	Q6S3E3	Q6se3 bacillus sp
39	49	62.8	713	1	CDG2_PAEMA	P31835 paenibacill
40	49	62.8	713	1	CDGT_BAC11	P30921 bacillus sp
41	49	62.8	713	1	CDGT_BACSO	P05618 bacillus sp
42	49	62.8	713	1	CDGT_BACS8	P17692 bacillus sp
43	49	62.8	713	1	CDGU_BACCI	P43379 bacillus ci
44	49	62.8	713	2	Q9FSW3	Q9fsw3 bacillus ci
45	49	62.8	718	1	CDGT_BACCI	P30920 bacillus ci

ALIGNMENTS

RESULT 1

ID	AMYA ASPAW	STANDARD;	PRT;	498 AA.
AC	Q02905;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Alpha-amylase A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase A).			
GN	Name=AMYA;			
OS	Aspergillus awamori.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Aspergillus.			
OC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.			
OX	NCBI_TaxID=105351;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=UVK143F;			
RX	MEDLINE=90254827; PubMed=2340591;			
RA	Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H., Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;			
RA	"Cloning, characterization, and expression of two alpha-amylase genes from Aspergillus niger var. awamori.";			
RT	Curr. Genet. 17:203-212(1990).			
RL				
CC	-I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.			
CC	-I- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory at high concentrations (By similarity).			
CC	-I- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.			
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CC	EMBL; X52755; CAA36966.1; -.			
CC	PIR; A48305; A48305.			
DR	HSP; P10529; 7TAA.			
DR	InterPro; IPR006589; Alp_amyl_cat_sub.			
DR	InterPro; IPR006047; Alpha_amyl_cat.			
DR	InterPro; IPR006046; Glyco_hydro_13.			
DR	Pfam; PF00128; Alpha-amylase; 1.			
DR	PRINTS; PR00110; ALPHAAMYLASE.			
DR	SMART; SM00642; Amy; 1.			
KW	Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;			
KW	Hydrolase; Multigene family; Signal.			
FT	SIGNAL 1 21 Potential.			
FT	CHAIN 22 498 Alpha-amylase A.			
FT	ACT SITE 227 227 Nucleophile (By similarity).			
FT	ACT_SITE 251 251 Proton donor (By similarity).			
FT	ACT_SITE 318 318 By similarity.			
FT	METAL 142 142 Calcium 1 (By similarity).			

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FT METAL      183      183      Calcium 1 (via carbonyl oxygen) (By
FT METAL      196      196      similarity)
FT METAL      227      227      Calcium 1 (By similarity)
FT METAL      231      231      Calcium 1 (via carbonyl oxygen) (By
FT METAL      251      251      similarity)
FT METAL      51       59       Calcium 2 (By similarity)
FT DISULFID   171      185       By similarity
FT DISULFID   261      304       By similarity
FT DISULFID   461      496       By similarity
FT CARBOHYD   218      218       N-linked (GlcNAc...) (Potential)
SQ SEQUENCE   498 AA; 54880 MW; 7659511BC01A8A01 CRC64;
Query Match      100.0%; Score 78; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
|||||
Db 99 AYHGYWQDDIYSL 111

RESULT 2
Q76CT3 PRELIMINARY; PRT; 498 AA.
ID Q76CT3
AC Q76CT3; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase.
GN Name:amylA;
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RA Ito K.;
CC Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB109452; BAD01051.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amyl; 1.
SQ SEQUENCE 498 AA; 54679 MW; 8407BBFC7F4E3FC0 CRC64;
Query Match      100.0%; Score 78; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
|||||
Db 98 AYHGYWQDDIYSL 110

RESULT 3
ID AMYA_ASPOR STANDARD; PRT; 499 AA.
AC P10529; P11763; Q00250;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase A precursor (EC 3.2.1.1) (Taka-amylase A) (TAA) (1,4-
DE Alpha-D-glucan glucanohydrolase).
GN Name:AMY1;
GN and
GN Name:AMY2;

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GN and
GN Name=AMY3;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 63303;
RX MEDLINE=89237897; PubMed=2785629;
RA Wirsel S., Lachmund A., Wildhardt G., Rutkowski E.;
RT "Three alpha-amylase genes of Aspergillus oryzae exhibit identical
RT intron-exon organization.";
RL Mol. Microbiol. 3:3-14(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6;
RA Genes M.J., Dove M.J., Seligy V.L.;
RT "Aspergillus oryzae has two nearly identical Taka-amylase genes, each
RT containing eight introns.";
RL Gene 79:107-117(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Tada S., Iimura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.;
RT "Cloning and nucleotide sequence of the genomic Taka-amylase A gene of
RT Aspergillus oryzae.";
RL Agric. Biol. Chem. 53:593-599(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
RA Takagoshi N., Furukawa M., Nagaba H., Kiritu N., Tauboi A., Uda S.;
RT "Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A:
RT evidence for multiple related genes.";
RL Gene 84:319-327(1989).
RN [5]
RP SEQUENCE OF 22-499.
RA Toda H., Kondo K., Narita K.;
RT "The complete amino acid sequence of Taka-amylase A.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 58:208-212(1982).
RN [6]
RP SEQUENCE OF 206-225.
RX MEDLINE=74001521; PubMed=4733850;
RA Isemura S., Ikenaka T.;
RT "The amino acid sequences of glycopeptides obtained from Taka-amylase
RT A with trypsin and chymotrypsin.";
RL J. Biochem. 74:1-10(1973).
RN [7]
RP SEQUENCE OF 433-499.
RA Narita K.;
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=80227691; PubMed=6156152;
RA Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
RA Toda H., Narita K., Kakudo M.;
RT "Molecular structure of taka-amylase A. I. Backbone chain folding at
RT 3-A resolution.";
RL J. Biochem. 87:1555-1558(1980).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=84212370; PubMed=6609921;
RA Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
RT "Structure and possible catalytic residues of Taka-amylase A.";
RL J. Biochem. 95:697-702(1984).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
RX MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
RA Brzozowski A.M., Davies G.J.;
RT "Structure of the Aspergillus oryzae alpha-amylase complexed with the
RT inhibitor acarbose at 2.0-A resolution.";
RL Biochemistry 36:10837-10845(1997).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.

```


RA Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
 RT "Cloning, characterization, and expression of two alpha-amylase genes
 from *Aspergillus niger* var. *awamori*.";
 RL Curr. Genet. 17:203-212(1990).
 CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides
 CC -|- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations (By similarity).
 CC -|- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X52756; CAA36967.1; -.
 CC FIR; B48305; B48305.
 CC HSP; P10529; 7TAA.
 CC InterPro; IPR006589; Alp_amy1_cat_sub.
 CC InterPro; IPR006047; Alpha_amy1_cat.
 CC InterPro; IPR006046; Glyco_hydro_13.
 CC Pfam; PF00128; Alpha-amylase; 1.
 CC PRINTS; PR00110; ALPHAAMYLASE.
 CC SMART; SM00642; Amy; 1.
 CC Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 CC Hydrolase; Multigene family; Signal.
 CC SIGNAL 1 21
 CC CHAIN 22 499 Alpha-amylase B.
 CC ACT_SITE 227 227 Nucleophile (By similarity).
 CC ACT_SITE 251 251 Proton donor (By similarity).
 CC ACT_SITE 318 318 By similarity.
 CC METAL 142 142 Calcium 1 (By similarity).
 CC METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
 CC similarity).
 CC METAL 196 196 Calcium 1 (By similarity).
 CC METAL 227 227 Calcium 2 (By similarity).
 CC METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
 CC similarity).
 CC METAL 251 251 Calcium 2 (By similarity).
 CC DISULFID 51 59 By similarity.
 CC DISULFID 171 185 By similarity.
 CC DISULFID 261 304 By similarity.
 CC DISULFID 461 496 By similarity.
 CC CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
 CC SEQUENCE 499 AA; 54921 MW; 740B96B11BC01A8A CRC64;
 CC -----
 CC Query Match 100.0%; Score 78; DB 1; Length 499;
 CC Best Local Similarity 100.0%; Pred. No. 0.00017;
 CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 1 AYHGWOODIYSL 13
 CC |||||
 CC DB 99 AYHGWOODIYSL 111

RESULT 5
 AMY_ASPSH
 ID -AMY_ASPSH STANDARD; PRT; 499 AA.
 AC P30292;
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE Glucanohydrolase).
 GN Name=AMY;
 OS *Aspergillus shirousami*.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.
 OX NCBI_TaxID=5070;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=92323146; PubMed=1368777;
 RA Shibuya I., Tamura G., Ishikawa T., Hara S.;
 RT "Cloning of the alpha-amylase cDNA of *Aspergillus shirousami* and its
 expression in *Saccharomyces cerevisiae*.";
 RL Biosci. Biotechnol. Biochem. 56:174-179(1992).
 CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides
 CC -|- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations (By similarity).
 CC -|- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D10461; BAA01255.1; -.
 CC HSP; P10529; 7TAA.
 CC InterPro; IPR006589; Alp_amy1_cat_sub.
 CC InterPro; IPR006047; Alpha_amy1_cat.
 CC InterPro; IPR006046; Glyco_hydro_13.
 CC Pfam; PF00128; Alpha-amylase; 1.
 CC PRINTS; PR00110; ALPHAAMYLASE.
 CC SMART; SM00642; Amy; 1.
 CC Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 CC Hydrolase; Signal.
 CC SIGNAL 1 21
 CC CHAIN 22 499 Alpha-amylase.
 CC ACT_SITE 227 227 Nucleophile (By similarity).
 CC ACT_SITE 251 251 Proton donor (By similarity).
 CC ACT_SITE 318 318 By similarity.
 CC METAL 142 142 Calcium 1 (By similarity).
 CC METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
 CC similarity).
 CC METAL 196 196 Calcium 1 (By similarity).
 CC METAL 227 227 Calcium 2 (By similarity).
 CC METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
 CC similarity).
 CC METAL 251 251 Calcium 2 (By similarity).
 CC DISULFID 51 59 By similarity.
 CC DISULFID 171 185 By similarity.
 CC DISULFID 261 304 By similarity.
 CC DISULFID 461 496 By similarity.
 CC CARBOHYD 218 218 N-linked (GlcNAc...) (By similarity).
 CC SEQUENCE 499 AA; 54852 MW; 1FB7AE50DA01C03F CRC64;
 CC -----
 CC Query Match 100.0%; Score 78; DB 1; Length 499;
 CC Best Local Similarity 100.0%; Pred. No. 0.00017;
 CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 1 AYHGWOODIYSL 13
 CC |||||
 CC DB 99 AYHGWOODIYSL 111

RESULT 6
 Q96TH4
 ID Q96TH4 PRELIMINARY; PRT; 499 AA.
 AC Q96TH4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Taka-amylase A (EC 3.2.1.1).
 GN Name=amyA;
 OS *Aspergillus oryzae*.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.
 OX NCBI_TaxID=5062;
 RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=RIB40;
RX MEDLINE=20289310; PubMed=10830498;
RA Gomi K., Akeno T., Minecoki T., Ozeki K., Kumagai C., Okazaki N.,
RA Iimura Y.;
RT "Molecular cloning and characterization of a transcriptional activator
RT gene, amyR, involved in the amylolytic gene expression in Aspergillus
RT oryzae.";
RL Biosci. Biotechnol. Biochem. 64:816-827(2000).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
EMBL; AB021876; BAA95703.1; -.
DR F01; JN0588; JN0588.
DR PIR; S04549; ALA83.
DR HSP; P10529; 7TAA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDDIYSL 13
Db |||||
99 AYHGYYQDDIYSL 111

RESULT 7
Q76L99 PRELIMINARY; PRT; 499 AA.
AC Q76L99;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase precursor.
GN Name=amy1;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT-11;
RA Matsubara T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
EMBL; AB083159; BAD06002.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 499 AA; 54794 MW; 2B357AE38B36C1C2 CRC64;

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDDIYSL 13
Db |||||
99 AYHGYYQDDIYSL 111

SEQUENCE FROM N.A.
Db 99 AYHGYYQDDIYSL 111
RESULT 8
Q7LV45 PRELIMINARY; PRT; 499 AA.
AC Q7LV45;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
GN Name=amy1;
OS Aspergillus flavus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5059;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=86-10D;
RA Fakhoury A.M., Woloshuk C.P.;
RL "Amy1, the alpha-amylase gene of Aspergillus flavus: Involvement in
RL aflatoxin biosynthesis in maize kernels.";
RL Phytopathology 89:908-914(1999).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
EMBL; AF139255; AAF14264.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDDIYSL 13
Db |||||
99 AYHGYYQDDIYSL 111

RESULT 9
Q9UV07 PRELIMINARY; PRT; 490 AA.
AC Q9UV07;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha-amylase AmyA.
GN Name=amyA;
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RC Roase N.A., Murphy R.M., Kelly J.M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
EMBL; AF208225; AAF17103.1; -.
DR HSP; P10529; 7TAA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.

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FT DISULFID 454 488      By similarity.
FT CARBOHYD 162      N-linked (GlcNAc...) (Potential).
FT CARBOHYD 357      N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 513 AA; 58715 MW; 455DD97FA428C182 CRC64;

Query Match      85.9%; Score 67; DB 1; Length 513;
Best Local Similarity 76.9%; Pred. No. 0.012;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYHGWOQDIYSL 13
Db 100 AYHGYPQDLVTL 112

RESULT 12
Q92394 ID Q92394 PRELIMINARY; PRT; 631 AA.
AC Q92394;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase precursor.
GN Name=amy-CS2;
OS Cryptococcus sp. S-2.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellomycetidae incertae sedis; Cryptococcus.
OX NCBI_TaxID=87049;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S-2;
RX MEDLINE=96433120; PubMed=8836148;
RA Iefuji H., Chino M., Kato M., Iimura Y.;
RT "Raw-starch-digesting and thermostable alpha-amylase from the yeast
RT Cryptococcus sp. S-2: purification, characterization, cloning, and
RT sequencing.";
RL Biochem. J. 318:989-996(1996).
DR EMBL; D83541; BAA1201.1; -
DR EMBL; D83540; BAA1201.1; -
DR PIR; S72270; S72270.
DR HSSP; P10529; 7TAA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR Pfam; PF00128; Alpha-amylase; 1.
DR Pfam; PF00686; CBM_20; 1.
DR ProDom; PD001568; Glyco_hydro_CBD; 1.
DR SMART; SM00642; Amy; 1.
DR SIGNAL.
FT CHAIN 1 20
FT SIGNAL 21 631 alpha-amylase.
SQ SEQUENCE 631 AA; 67658 MW; 8196B7B61D707B5 CRC64;

Query Match      84.6%; Score 66; DB 2; Length 631;
Best Local Similarity 76.9%; Pred. No. 0.022;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AYHGWOQDIYSL 13
Db 105 AYHGYPQDIYSL 117

RESULT 13
AMYA ASPNG ID AMYA ASPNG STANDARD; PRT; 484 AA.
AC P56271;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acid alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;

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RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RP MEDLINE=91002514; PubMed=2207069;
RX Boel E., Brady L., Brzozowski A.M., Derewenda Z., Dodson G.G.,
RA Jensen V.J., Petersen S.B., Swift H., Thim L., Woldike H.P.;
RT "Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-
RT A resolution of two enzymes from Aspergillus.";
RL Biochemistry 29:6244-6249(1990).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COPACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC PDB; 2AAA; X-ray; @=1-484.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; Alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW 3D-structure; Calcium-binding; Carbohydrate metabolism; Glycoprotein;
KW Glycosidase; Hydrolase.
FT ACT_SITE 206 206 Nucleophile.
FT ACT_SITE 230 230 Proton donor.
FT ACT_SITE 297 297
FT METAL 121 121 Calcium 1.
FT METAL 162 162 Calcium 1 (via carbonyl oxygen).
FT METAL 175 175 Calcium 1.
FT METAL 206 206 Calcium 2.
FT METAL 210 210 Calcium 1 (via carbonyl oxygen).
FT METAL 230 230 Calcium 2.
FT DISULFID 30 38
FT DISULFID 150 164
FT DISULFID 240 283
FT DISULFID 440 475
FT CARBOHYD 24 24 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 157 157 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 197 197 N-linked (GlcNAc...) (Potential).
FT HELIX 3 6
FT TURN 7 8
FT STRAND 11 13
FT HELIX 16 19
FT TURN 22 23
FT HELIX 32 34
FT HELIX 42 47
FT TURN 48 48
FT HELIX 49 53
FT TURN 54 56
FT TURN 59 62
FT STRAND 66 68
FT STRAND 73 73
FT TURN 74 75
FT STRAND 76 76
FT TURN 79 80
FT STRAND 84 90
FT TURN 92 94
FT HELIX 97 108
FT TURN 109 111
FT STRAND 113 118
FT STRAND 122 122
FT STRAND 125 125
FT HELIX 129 131
FT HELIX 134 136
FT STRAND 138 138
FT HELIX 143 145
FT STRAND 146 146
FT STRAND 151 151
FT TURN 155 156
FT HELIX 158 163
FT STRAND 165 167
FT STRAND 172 173
FT STRAND 175 176
FT TURN 178 179
FT HELIX 181 181

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FT TURN 199 205 199
FT TURN 202 205 202
FT TURN 209 210 209
FT TURN 213 215 213
FT TURN 216 223 216
FT TURN 224 224 224
FT TURN 226 229 226
FT TURN 236 239 236
FT TURN 240 244 240
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FT TURN 248 250 248
FT TURN 252 262 252
FT TURN 265 266 265
FT TURN 269 282 269
FT TURN 286 288 286
FT TURN 290 291 290
FT TURN 296 297 296
FT TURN 301 303 301
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FT TURN 419 423 419
FT TURN 430 431 430
FT TURN 433 436 433
FT TURN 437 440 437
FT TURN 441 444 441
FT TURN 447 448 447
FT TURN 451 455 451
FT TURN 457 458 457
FT TURN 461 465 461
FT TURN 466 469 466
FT TURN 470 471 470
FT TURN 474 475 474
SQ SEQUENCE 484 AA; 52935 MW; 04D596E34680656D CRC64;

Query Match 82.1%; Score 64; DB 1; Length 484;
Best Local Similarity 76.9%; Pred. No. 0.035; 2; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 2;

QY 1 AYHGYWQDIYSL 13
Db 78 AYHGYWQDIYDV 90

RESULT 14
AMY2 DEBOC
ID AMY2 DEBOC STANDARD; PRT; 507 AA.
AC Q08806;
DT 29-MAR-2004 (Rel. 43, Created)
DT 25-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase 2 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE Glucanohydrolase 2).
GN Name=SWA2;
OS Debaryomyces occidentalis (Yeast) (Schwanniomyces occidentalis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OC NCBI_TaxID=27300;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 26077 / CBS 2863;
RX MEDLINE=93365041; PubMed=8358835;
RA "Molecular structure of the SWA2 gene encoding an AMY1-related alpha-
RT amylase from Schwanniomyces occidentalis.";
RL Curr. Genet. 24:75-83(1993).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X73497; CAAS1912.1; -.
DR PIR; S33921; S33921.
DR HSP; P10529; 7TAA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Aamy; 1.
DR KEGG; K01101; Carbohydrate metabolism; Glycoprotein; Glycosidase;
KW Hydrolase; Signal.
FT SIGNAL 1 20
FT CHAIN 21 507
FT ACT_SITE 238 238
FT ACT_SITE 262 262
FT ACT_SITE 329 329
FT METAL 153 153
FT METAL 194 194
FT METAL 207 207
FT METAL 238 238
FT METAL 242 242
FT METAL 262 262
FT DISULFID 62 70
FT DISULFID 182 196
FT DISULFID 272 315
FT DISULFID 470 505
FT CARBOHYD 229 229
SQ SEQUENCE 507 AA; 55966 MW; 3A562E95BD8AD63 CRC64;

Query Match 82.1%; Score 64; DB 1; Length 507;
Best Local Similarity 69.2%; Pred. No. 0.037; 3; Mismatches 1; Indels 0; Gaps 0;
Matches 9; Conservative 3;

QY 1 AYHGYWQDIYSL 13
Db 110 AYHGYWQDIYAI 122

RESULT 15
Q76L96
ID Q76L96 PRELIMINARY; PRT; 634 AA.
AC Q76L96;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase precursor.
DE Name=amy1 III;
GN Aspergillus awamori.
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Aspergillaceae; Aspergillus.
OC NCBI_TaxID=105351;
OX NCBI_TaxID=105351;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT-11;
RA Matsubara T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083162; BAD06005.1; -
DR EMBL; AB083160; BAD06003.1; -
DR HSSP; P04064; 1ACZ.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR002044; Glyco_hydro_CBD.
DR Pfam; PF00128; Alpha-amylase; 1.
DR Pfam; PF00686; CBM_20; 1.
DR ProDom; PD001568; Glyco_hydro_CBD; 1.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 1 21 Potential.
      1 21 16C0BE6AF6FE0E9B CRC64;

Query Match      82.1%; Score 64; DB 2; Length 634;
Best Local Similarity 76.9%; Pred. No. 0.047;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AYHGTYQDIYSL 13
Db 99 AYHGYWQQKIYDV 111

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Search completed: November 7, 2005, 18:52:30
 Job time : 7.97683 secs

The Page Book (1904)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 17:47:24 ; Search time 1.95733 Seconds
(without alignments)
495.746 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110

Perfect score: 78

Sequence: 1 AYHGYWQDIYSL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	478	1	US-08-720-899-7
2	78	100.0	478	1	US-08-459-610-7
3	78	100.0	478	2	US-08-343-804-7
4	78	100.0	478	2	US-08-600-908A-10
5	78	100.0	478	3	US-08-683-838A-10
6	78	100.0	478	3	US-09-182-859-7
7	78	100.0	478	4	US-09-672-459-7
8	78	100.0	478	4	US-09-636-252A-10
9	78	100.0	478	4	US-10-186-042-7
10	62	79.5	478	2	US-08-339-715A-2
11	54	69.2	468	1	US-08-204-656B-2
12	54	69.2	468	1	US-08-470-702-6
13	54	69.2	468	1	US-08-467-831-6
14	53	67.9	468	1	US-08-204-656B-4
15	53	67.9	468	1	US-08-470-702-7
16	53	67.9	468	1	US-08-467-831-7
17	50	64.1	468	1	US-08-204-656B-6
18	50	64.1	468	1	US-08-470-702-8
19	50	64.1	468	1	US-08-467-831-8
20	49	62.8	468	1	US-08-204-656B-8
21	49	62.8	468	1	US-08-470-702-9
22	49	62.8	468	1	US-08-467-831-9
23	49	62.8	685	3	US-08-947-965-72
24	49	62.8	685	3	US-08-947-965-74
25	49	62.8	686	3	US-08-947-965-70
26	49	62.8	686	3	US-08-947-965-73
27	47	60.3	624	3	US-08-947-965-78

28	47	60.3	655	1	US-08-469-202-27	Sequence 27, Appl
29	47	60.3	655	1	US-08-469-202-28	Sequence 28, Appl
30	47	60.3	655	2	US-08-484-434C-34	Sequence 34, Appl
31	47	60.3	655	2	US-08-484-434C-35	Sequence 35, Appl
32	47	60.3	655	4	US-09-384-361-34	Sequence 34, Appl
33	47	60.3	655	4	US-09-384-361-35	Sequence 35, Appl
34	46	59.0	675	3	US-08-947-965-76	Sequence 76, Appl
35	46	59.0	676	3	US-08-947-965-71	Sequence 71, Appl
36	46	59.0	680	3	US-08-947-965-77	Sequence 77, Appl
37	46	59.0	683	3	US-08-947-965-2	Sequence 2, Appl
38	46	59.0	687	3	US-08-947-965-75	Sequence 75, Appl
39	46	59.0	725	2	US-08-816-105A-1	Sequence 1, Appl
40	45	57.7	719	3	US-09-386-607-2	Sequence 2, Appl
41	45	57.7	719	4	US-09-645-707B-2	Sequence 2, Appl
42	44	56.4	14	1	US-08-204-656B-11	Sequence 11, Appl
43	44	56.4	14	1	US-08-470-702-11	Sequence 11, Appl
44	44	56.4	14	1	US-08-467-831-11	Sequence 11, Appl
45	44	56.4	454	1	US-07-930-686-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-08-720-899-7

; Sequence 7, Application US/08720899

; Patent No. 5753460

; GENERAL INFORMATION:

; APPLICANT: Bisgaard-Frantzen, Henrik

; APPLICANT: Borchert, Torben Vedel

; APPLICANT: Svendsen, Allan

; APPLICANT: Thellersen, Marianne

; APPLICANT: Van der Zee, Pia

; TITLE OF INVENTION: AMYLASE VARIANTS

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 5753460o No. 5753460disk of No. 5753460th America, Inc.

; STREET: 405 Lexington Avenue, 64th Floor

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/720,899

; FILING DATE: 10-OCT-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/343,804

; FILING DATE: 22-NOV-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lowney Dr., Karen A.

; REGISTRATION NUMBER: 31,274

; REFERENCE/DOCKET NUMBER: 4054.214-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 478 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-720-899-7

Query Match 100.0%; Score 78; DB 1; Length 478;

Best Local Similarity 100.0%; Pred. No. 0.00012; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0;

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QY 1 AYHGYYQDDIYSL 13
Db 78 AYHGYYQDDIYSL 90

RESULT 2
US-08-459-610-7
; Sequence 7, Application US/08459610
; Patent No. 5801043
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5801043o No. 5801043disk of No. 5801043th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,610
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-459-610-7

Query Match 100.0%; Score 78; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYYQDDIYSL 13
Db 78 AYHGYYQDDIYSL 90

RESULT 3
US-08-343-804-7
; Sequence 7, Application US/08343804
; Patent No. 5830837
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5830837o No. 5830837disk of No. 5830837th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-600-908A-10

Query Match      100.0%; Score 78; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYWQDDIYSL 13
Db      78 AYHGYWQDDIYSL 90

RESULT 5
US-08-683-838A-10
; Sequence 10, Application US/08683838A
; Patent No. 6022724
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: "-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 60227240 No. 6022724disk of No. 6022724th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,838A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-683-838A-10

Query Match      100.0%; Score 78; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYWQDDIYSL 13
Db      78 AYHGYWQDDIYSL 90

RESULT 6
US-09-182-859-7
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; Sequence 7, Application US/09182859
; Patent No. 6143708
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/182,859
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: 0515/96
; EARLIER FILING DATE: 1996-04-30
; EARLIER APPLICATION NUMBER: 0712/96
; EARLIER FILING DATE: 1996-06-28
; EARLIER APPLICATION NUMBER: 0775/96
; EARLIER FILING DATE: 1996-07-11
; EARLIER APPLICATION NUMBER: 1263/96
; EARLIER FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-182-859-7

Query Match      100.0%; Score 78; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYWQDDIYSL 13
Db      78 AYHGYWQDDIYSL 90

RESULT 7
US-09-672-459-7
; Sequence 7, Application US/09672459
; Patent No. 6436888
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/672,459
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-672-459-7

Query Match      100.0%; Score 78; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYWQDDIYSL 13
Db      78 AYHGYWQDDIYSL 90
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RESULT 8
US-09-636-252A-10
; Sequence 10, Application US/09636252A
; Patent No. 6440716
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/09/636,252A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-09-636-252A-10

Query Match 100.0%; Score 78; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
Db 78 AYHGYWQDIYSL 90

RESULT 9
US-10-186-042-7
; Sequence 7, Application US/10186042
; Patent No. 6642044
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match 100.0%; Score 78; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
Db 78 AYHGYWQDIYSL 90

RESULT 10
US-08-339-715A-2
; Sequence 2, Application US/08339715A
; Patent No. 5965442
; GENERAL INFORMATION:
; APPLICANT: Kaneko, Hiroki
; APPLICANT: Takada, Toshikazu
; APPLICANT: Shimada, Jiro
; APPLICANT: Kuriki, Takashi
; APPLICANT: Yanase, Michiyo
; APPLICANT: Takata, Hiroki
; APPLICANT: Okada, Shigetaka
; TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
; TITLE OF INVENTION: NEOPULLULANASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
; STREET: Metropolitan Square Building, Suite 800, 1450
; STREET: G. Street
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,715A
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306096/1993
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Melser, Allen S.
; REGISTRATION NUMBER: 27,215
; REFERENCE/DOCKET NUMBER: 18335.009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-824-8000
; TELEFAX: 202-824-8199
; TELEX: 248516
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-339-715A-2

Query Match 79.5%; Score 62; DB 2; Length 478;
Best Local Similarity 84.6%; Pred. No. 0.044;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
Db 78 AYTYWQTDIYSL 90

RESULT 11
US-08-204-656B-2
; Sequence 2, Application US/08204656B
; Patent No. 5538882
; GENERAL INFORMATION:
; APPLICANT: Matsui, Ikuro
; APPLICANT: Ishikawa, Kazuhiko
; APPLICANT: Miyairi, Sachio
; APPLICANT: Honda, Koichi
; TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
; TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
; TITLE OF INVENTION: Oligosaccharide Using The Enzyme
```

NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,656B
FILING DATE: 02-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weiner, Marc S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-204-656B-2

Query Match 69.2%; Score 54; DB 1; Length 468;
Best Local Similarity 53.8%; Pred. No. 0.82;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AYHGWOODIYSL 13
Db 79 AYHGFWMKNIYKI 91

RESULT 12
US-08-470-702-6
Sequence 6, Application US/08470702
Patent No. 5631149
GENERAL INFORMATION:
APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656

FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-470-702-6
Query Match 69.2%; Score 54; DB 1; Length 468;
Best Local Similarity 53.8%; Pred. No. 0.82;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AYHGWOODIYSL 13
Db 79 AYHGFWMKNIYKI 91

RESULT 13
US-08-467-831-6
Sequence 6, Application US/08467831
Patent No. 5635378
GENERAL INFORMATION:
APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,831
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-467-831-6

Query Match 69.2%; Score 54; DB 1; Length 468;
Best Local Similarity 53.8%; Pred. No. 0.82; Mismatches 4; Indels 2; Gaps 0;
Matches 7; Conservative

QY 1 AYHGWOQDIYSL 13
|||||:|:|:
Db 79 AYHGWWMKIYKI 91

RESULT 14

US-08-204-656B-4
; Sequence 4, Application US/08204656B
; Patent No. 5538882

; GENERAL INFORMATION:
; APPLICANT: Matsui, Ikuro
; APPLICANT: Ishikawa, Kazuhiko
; APPLICANT: Miyairi, Sachio
; APPLICANT: Honda, Koichi
; TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
; TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
; TITLE OF INVENTION: Oligosaccharide Using The Enzyme
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/204,656B
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiner, Marc S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-204-656B-4

Query Match 67.9%; Score 53; DB 1; Length 468;
Best Local Similarity 53.8%; Pred. No. 1.2; Mismatches 4; Indels 2; Gaps 0;
Matches 7; Conservative

QY 1 AYHGWOQDIYSL 13
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Db 79 AYHGWWMKIYKI 91

RESULT 15

US-08-470-702-7
; Sequence 7, Application US/08470702

; Patent No. 5631149
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKURO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
; TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
; TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
; TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/470,702
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/204,656
; FILING DATE: 02-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-470-702-7

Query Match 67.9%; Score 53; DB 1; Length 468;
Best Local Similarity 53.8%; Pred. No. 1.2; Mismatches 4; Indels 2; Gaps 0;
Matches 7; Conservative

QY 1 AYHGWOQDIYSL 13
|||||:|:|:
Db 79 AYHGWWMKIYKI 91

Search completed: November 7, 2005, 18:25:06
Job time: 1.95753 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:11:05 ; Search time 7.05212 Seconds
(without alignments)
771.303 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110

Perfect score: 78

Sequence: 1 AYHGYYQDIYSL 13

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Searched: 1867879 seqs, 418409474 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	78	100.0	478	14	US-10-184-771-10
3	78	100.0	478	14	US-10-186-042-7
4	78	100.0	478	15	US-10-644-187-7
5	78	100.0	478	17	US-10-526-720-10
6	78	100.0	478	17	US-10-980-759-7
7	78	100.0	478	20	US-11-064-196-10
8	78	100.0	498	16	US-10-815-495-22
9	78	100.0	498	16	US-10-820-200-2
10	78	100.0	498	17	US-10-877-849-30
11	78	100.0	499	16	US-10-815-495-18
					Sequence 43, Appl
					Sequence 10, Appl
					Sequence 7, Appl
					Sequence 7, Appl
					Sequence 10, Appl
					Sequence 7, Appl
					Sequence 10, Appl
					Sequence 22, Appl
					Sequence 2, Appl
					Sequence 30, Appl
					Sequence 18, Appl

12	78	100.0	499	16	US-10-797-393A-5	Sequence 5, Appl
13	78	100.0	608	17	US-10-877-849-40	Sequence 40, Appl
14	78	100.0	640	17	US-10-877-849-36	Sequence 36, Appl
15	78	100.0	1095	14	US-10-228-063-45	Sequence 45, Appl
16	75	96.2	495	14	US-10-213-990-42	Sequence 42, Appl
17	70	89.7	494	17	US-10-486-868-13	Sequence 13, Appl
18	69	88.5	500	15	US-10-369-493-12469	Sequence 12469, A
19	67	85.9	513	15	US-10-369-493-2223	Sequence 2223, Ap
20	65	83.3	547	14	US-10-213-990-48	Sequence 48, Appl
21	64	82.1	484	15	US-10-416-393-1	Sequence 1, Appl
22	64	82.1	484	16	US-10-797-393A-1	Sequence 1, Appl
23	64	82.1	505	17	US-10-877-849-42	Sequence 42, Appl
24	64	82.1	511	17	US-10-877-849-8	Sequence 8, Appl
25	64	82.1	609	17	US-10-877-849-38	Sequence 38, Appl
26	64	82.1	629	17	US-10-877-849-34	Sequence 34, Appl
27	64	82.1	640	17	US-10-877-849-32	Sequence 32, Appl
28	63	80.8	555	17	US-10-877-849-15	Sequence 15, Appl
29	63	80.8	567	17	US-10-486-868-18	Sequence 18, Appl
30	63	80.8	640	17	US-10-877-007-22	Sequence 22, Appl
31	63	80.8	640	17	US-10-877-849-41	Sequence 41, Appl
32	58	74.4	630	14	US-10-213-990-45	Sequence 45, Appl
33	57	73.1	263	16	US-10-425-115-291647	Sequence 291647, A
34	57	73.1	549	17	US-10-486-868-14	Sequence 14, Appl
35	56	71.8	493	15	US-10-369-493-22723	Sequence 22723, A
36	53	67.9	564	15	US-10-369-493-22679	Sequence 22679, A
37	52	66.7	711	16	US-10-474-792-22	Sequence 22, Appl
38	49	62.8	686	17	US-10-872-198-44	Sequence 44, Appl
39	49	62.8	686	17	US-10-872-197A-44	Sequence 44, Appl
40	49	62.8	686	18	US-10-787-219A-52	Sequence 52, Appl
41	49	62.8	686	20	US-11-021-951-44	Sequence 44, Appl
42	49	62.8	713	17	US-10-504-543-4	Sequence 4, Appl
43	48	61.5	502	14	US-10-081-872-108	Sequence 108, App
44	48	61.5	502	15	US-10-385-305-108	Sequence 108, App
45	47	60.3	483	15	US-10-369-493-597	Sequence 597, App

ALIGNMENTS

RESULT 1

US-10-877-849-43

; Sequence 43, Application US/10877849

; Publication No. US20050054071A1

; GENERAL INFORMATION:

; APPLICANT: Udagawa, Hiroaki

; APPLICANT: Taira, Rikako

; APPLICANT: Tkagi, Shinobu

; APPLICANT: Allain, Eric

; APPLICANT: Hjort, Carsten

; APPLICANT: Vikso-Nielsen, Anders

; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING

; FILE REFERENCE: 10490.500-US

; CURRENT APPLICATION NUMBER: US/10/877,849

; CURRENT FILING DATE: 2004-06-25

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 43

; LENGTH: 476

; TYPE: PRT

; ORGANISM: Aspergillus oryzae

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: (1)..(476)

US-10-877-849-43

Query Match 100.0%; Score 78; DB 17; Length 476;

Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDIYSL 13

Db 78 AYHGYYQDIYSL 90

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RESULT 2
US-10-184-771-10
; Sequence 10, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-10-184-771-10

Query Match          100.0%; Score 78; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVHGYWQDDIYSL 13
Db 78 AVHGYWQDDIYSL 90

RESULT 3
US-10-186-042-7
; Sequence 7, Application US/10186042
; Publication No. US20030171236A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match          100.0%; Score 78; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVHGYWQDDIYSL 13
Db 78 AVHGYWQDDIYSL 90

RESULT 4
US-10-644-187-7
; Sequence 7, Application US/10644187
; Publication No. US20040048351A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/644,187
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-644-187-7

Query Match          100.0%; Score 78; DB 15; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVHGYWQDDIYSL 13
Db 78 AVHGYWQDDIYSL 90

RESULT 5
US-10-926-720-10
; Sequence 10, Application US/10926720
; Publication No. US20050019886A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg+rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/926,720
; FILING DATE: 26-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
```


REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10

Query Match 100.0%; Score 78; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDDIYSL 13
|||||
Db 78 AYHGYWQDDIYSL 90

RESULT 6

US-10-980-759-7
Sequence 7, Application US/10980759
Publication No. US20050118693A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/980,759
CURRENT FILING DATE: 2004-11-03
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Fast-SEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 478
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-980-759-7

Query Match 100.0%; Score 78; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDDIYSL 13
|||||
Db 78 AYHGYWQDDIYSL 90

RESULT 7

US-11-064-196-10
Sequence 10, Application US/11064196
Publication No. US20050170487A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants

FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/11/064,196
CURRENT FILING DATE: 2005-02-22
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Fast-SEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 478
TYPE: PRT
ORGANISM: A. oryzae
US-11-064-196-10

Query Match 100.0%; Score 78; DB 20; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDDIYSL 13
|||||
Db 78 AYHGYWQDDIYSL 90

RESULT 8

US-10-815-495-22
Sequence 22, Application US/10815495
Publication No. US20040191864A1
GENERAL INFORMATION:
APPLICANT: Novozymes Biotech, Inc.
APPLICANT: Connelly, Mariah
APPLICANT: Brody, Howard
TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
TITLE OF INVENTION: Mutants Of Aspergillus Niger
FILE REFERENCE: 10345.200-US
CURRENT APPLICATION NUMBER: US/10/815,495
CURRENT FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 498
TYPE: PRT
ORGANISM: Aspergillus niger
US-10-815-495-22

Query Match 100.0%; Score 78; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDDIYSL 13
|||||
Db 99 AYHGYWQDDIYSL 111

RESULT 9

US-10-820-200-2
Sequence 2, Application US/10820200
Publication No. US20040229764A1
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Pedersen, Sven
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
FILE REFERENCE: 5835.200-US
CURRENT APPLICATION NUMBER: US/10/820,200
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US/09/710,339
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/165,786
PRIOR FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2

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; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus Oryzae
US-10-820-200-2

Query Match      100.0%; Score 78; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
|||||
DB 98 AYHGYWQDIYSL 110

RESULT 10
US-10-877-849-30
; Sequence 30, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-877-849-30

Query Match      100.0%; Score 78; DB 17; Length 498;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
|||||
DB 98 AYHGYWQDIYSL 110

RESULT 11
US-10-815-495-18
; Sequence 18, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connolly, Marian
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; TITLE OF INVENTION: Mutants Of Aspergillus Niger
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-18

Query Match      100.0%; Score 78; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
|||||
DB 98 AYHGYWQDIYSL 110

RESULT 12
US-10-797-393A-5
; Sequence 5, Application US/10797393A
; Publication No. US20040219649A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Hans Sejr
; APPLICANT: Pedersen, Sven
; APPLICANT: Festeren, Rikke Monica
; TITLE OF INVENTION: ALCOHOL PRODUCT PROCESSES
; FILE REFERENCE: 10391.200-US
; CURRENT APPLICATION NUMBER: US/10/797,393A
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-797-393A-5

Query Match      100.0%; Score 78; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
|||||
DB 98 AYHGYWQDIYSL 111

RESULT 13
US-10-877-849-40
; Sequence 40, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-40

Query Match      100.0%; Score 78; DB 17; Length 608;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
|||||
DB 98 AYHGYWQDIYSL 110

RESULT 14
US-10-877-849-36
; Sequence 36, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
```

; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-36

Query Match 100.0%; Score 78; DB 17; Length 640;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
| | | | | | | | | | | | | | |
Db 98 AYHGYWQDIYSL 110

RESULT 15
US-10-228-063-45
; Sequence 45, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lahanan, Mike
; TITLE OF INVENTION: Self-processing Plants and Plant Parts
; FILE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228.063
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Aspergillus shirousami
US-10-228-063-45

Query Match 100.0%; Score 78; DB 14; Length 1095;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
| | | | | | | | | | | | | | |
Db 78 AYHGYWQDIYSL 90

Search completed: November 7, 2005, 18:45:03
Job time : 8.05212 secs

The Page Pink (copy)

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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:58:55 ; Search time 7.47876 Seconds
(without alignments)
672.288 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110
Perfect score: 13
Sequence: 1 AYHGYWQDIYSL 13

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	478	2 AAR46065	Mutant al
2	13	100.0	478	2 AAR72450	Aspergill
3	13	100.0	478	2 AAR78270	Aspergill
4	13	100.0	478	2 AAW14500	Aspergill
5	13	100.0	498	4 AAB84206	Amino aci
6	13	100.0	498	8 AAB84206	Amino aci
7	13	100.0	499	8 ADT89632	Aspergill
8	13	100.0	1095	6 ADT89628	Aspergill
9	12	92.3	495	6 ABP96630	Alpha-amy
10	11	84.6	423	4 ABB80177	A. fumiga
11	9	69.2	494	6 ABB09072	Aspergill
12	8	61.5	484	5 ABP97894	Amino aci
13	8	61.5	484	8 AAE24207	Aspergill
14	7	53.8	630	8 ADS75939	Aspergill
15	6	46.2	31	2 ABB80178	A. fumiga
16	6	46.2	55	2 AAR85808	Peptide r
17	6	46.2	429	8 AAR88213	Alpha-amy
18	6	46.2	429	8 ADS44209	Bacterial
19	6	46.2	468	2 AAR24136	Alpha-amy
20	6	46.2	493	2 AAR88212	Bacterial
21	6	46.2	493	8 ADS44293	Bacterial
22	6	46.2	494	1 AAP70571	Alpha-amy
23	6	46.2	500	8 ADS23436	Bacterial
24	6	46.2	511	1 AAP81161	Recombina
25	6	46.2	511	1 AAP81180	Sequence

26	6	46.2	512	2 AAR07574	Alpha-amy
27	6	46.2	513	8 ADN19570	Bacterial
28	6	46.2	514	2 AAW84268	Candida a
29	6	46.2	547	6 ABB80179	A. fumiga
30	6	46.2	549	6 ABP97895	Amino aci
31	6	46.2	555	6 ABP97896	Amino aci
32	6	46.2	564	8 ADS44249	Bacterial
33	6	46.2	567	6 ABP97899	Amino aci
34	6	46.2	567	6 ABP97899	Sequence
35	6	46.2	586	1 AAP61518	Sequence
36	6	46.2	586	2 AAW17605	Bacillus
37	6	46.2	586	2 AAW17600	Bacillus
38	6	46.2	586	2 AAW17603	Bacillus
39	6	46.2	586	2 AAW17592	Bacillus
40	6	46.2	586	2 AAW17596	Bacillus
41	6	46.2	586	2 AAW06773	Wild type
42	6	46.2	586	2 AAW17599	Bacillus
43	6	46.2	586	2 AAW17594	Bacillus
44	6	46.2	586	2 AAW17595	Bacillus
45	6	46.2	586	2 AAW17593	Bacillus

ALIGNMENTS

RESULT 1
AAR46065
ID AAR46065 standard; protein; 478 AA.
XX
AC AAR46065;
XX
DT 25-MAR-2003 (revised)
DT 18-JUL-1994 (first entry)
XX
DE Mutant alpha-amyase.
XX
KW Methionine substitution; stability; activity; detergent;
KW dishwashing agents; liquifaction agents.
XX
OS Aspergillus oryzae.
XX
PN WO9402597-A1.
XX
PD 03-FEB-1994.
XX
PF 06-JUL-1993; 93WO-DK000230.
XX
PR 23-JUL-1992; 92DK-00000946.
PR 16-DEC-1992; 92DK-00001503.
PR 15-MAR-1993; 93DK-00000292.
(NOVO) NOVO-NORDISK AS.
Svendsen A, Bisgaard-Frantzen H;
WPI; 1994-048855/06.
XX
DR Mutant alpha-amyase from Bacillus species comprising a methionine
XX substitution - with improved stability and activity at low pH, for use in
PT detergents, dishwashing agents and liquifaction agents.
PT
XX
PS Claim 1; Page 7; 20pp; English.
XX
CC The sequence os that of the Asoergillus oryzae alpha amylase, sold
CC commercially as FUNGAMYL (TM) by Novo Nordisk A/S. The sequence can be
CC mutated by substitution of one or more of its methionine residues for any
CC amino acid other than cysteine. The mutant alpha-amyase exhibits a
CC better activity level and better stability in the presence of oxidising
CC agents than previous mutant alpha amylases, and improved thermostability
CC at moderately low pH. The enzyme can be used as an additive for
CC detergents, dishwashing agents and liquifaction agents. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX

```

SQ Sequence 478 AA;
  Query Match          100.0%; Score 13; DB 2; Length 478;
  Best Local Similarity 100.0%; Pred. No. 2e-06;
  Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
Db 78 AYHGYWQDDIYSL 90

RESULT 2
AAR72450
ID AAR72450 standard; protein; 478 AA.
XX
AC AAR72450;
XX
DT 25-MAR-2003 (revised)
DT 01-DEC-1995 (first entry)
XX
DE Aspergillus oryzae alpha amylase (mature protein).
XX
KW Alpha amylase; variant; enzyme; detergent; additive; dishwashing;
KW washing; Bacillus licheniformis; Bacillus amyloliquefaciens;
KW Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
KW thermostable.
XX
OS Aspergillus oryzae.
XX
FN WO9510603-A1.
XX
PD 20-APR-1995.
XX
PF 05-OCT-1994; 94WO-DK000370.
XX
PR 08-OCT-1993; 93DK-00001133.
XX
PR 02-FEB-1994; 94DK-00000140.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Borchert TV, Bisgard-Frantzen H, Svendsen A, Thellersen M;
PI Van Der Zee P;
XX
DR WPI; 1995-161790/21.
XX
PT New Bacillus derived alpha-amylase variants - having amino acid
PT modifications to improve washing and/or dishwashing performance.
XX
PS Disclosure; Page 75-76; 105pp; English.
XX
CC Variant alpha amylase enzymes which have improved washing and/or as
CC detergent additives. The enzymes have one or more amino acid residues
CC added, deleted or substituted. The variants can also be used for textile
CC desizing prior to scouring, bleaching and dyeing. The variants have
CC improved thermostability, acid/alkaline stability; low temperature
CC optimum; pH optimum; higher hydrolysis velocity and improved tolerance to
CC other composition constituents, e.g. oxidation agents. (Updated on 25-MAR
CC -2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 478 AA;
  Query Match          100.0%; Score 13; DB 2; Length 478;
  Best Local Similarity 100.0%; Pred. No. 2e-06;
  Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
Db 78 AYHGYWQDDIYSL 90

RESULT 3
AAR78270
ID AAR78270 standard; protein; 478 AA.
XX
AC AAR78270;
XX
DT 17-JAN-1996 (first entry)
XX
DE Aspergillus oryzae alpha amylase (mature protein).
XX
KW Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch;
KW thermostable; methionine; Bacillus licheniformis;
KW Bacillus amyloliquefaciens; Bacillus stearothermophilus;
KW Aspergillus oryzae.
XX
OS Aspergillus oryzae.
XX
FN WO9521247-A1.
XX
PD 10-AUG-1995.
XX
PF 05-OCT-1994; 94WO-DK000371.
XX
PR 02-FEB-1994; 94DK-00000141.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Toft AH, Marcher D, Pedersen HH, Nilsson TE;
XX
DR WPI; 1995-283767/37.
XX
PT Use of an oxidation stable alpha-amylase - for simultaneous desizing and
PT bleaching or scouring of fabrics contg. starch or starch derivs.
XX
PS Disclosure; Page 25-26; 37pp; English.
XX
CC Oxidation stable alpha amylases can be used for the simultaneous desizing
CC and bleaching or scouring of a fabric comprising starch or starch
CC derivatives. They exhibit a better heat stability, especially in the
CC presence of oxidising agents. They are obtained from a parent alpha
CC amylase by replacing one or more methionine residues with any amino acid
CC different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or
CC Asp. The parent alpha amylase is pref. derived from a Bacillus species,
CC although alpha amylases of fungal origin can also be used. This sequence
CC is the wild type (unmodified) alpha amylase of Aspergillus oryzae
XX
SQ Sequence 478 AA;
  Query Match          100.0%; Score 13; DB 2; Length 478;
  Best Local Similarity 100.0%; Pred. No. 2e-06;
  Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
Db 78 AYHGYWQDDIYSL 90

RESULT 4
AAW14500
ID AAW14500 standard; protein; 478 AA.
XX
AC AAW14500;
XX
DT 04-JUN-1997 (first entry)
XX
DE Aspergillus oryzae alpha-amylase (mature protein).
XX
KW alpha-amylase; mature; Bacillus licheniformis; termamyl; fungamyl;
KW Aspergillus oryzae; Bacillus amyloliquefaciens; altered property;
KW calcium dependency; substrate binding; stability; pH optimum;
KW thermostability; cleavage; oligosaccharide substrate; dishwashing;
KW washing; detergent additive; fabric desizing; starch liquefaction;
KW sweetener; ethanol production; variant.
XX
OS Aspergillus oryzae.
XX
```

PH	Key	Location/Qualifiers
FT	Misc-difference	13. .45
FT		/label= loop 1 modification region
FT		/note= "at least one amino acid residue of a parent alpha
FT		-amylase (used as a template for a variant) corresponding
FT		to 7-23 of AAW14499 is deleted or replaced with a
FT		fragment corresponding to this fragment; claim 33"
FT	Misc-difference	14. .40
FT		/label= loop 1 modification region
FT		/note= "preferred region where at least one amino acid
FT		residue of a parent alpha-amylase (used as a template for
FT		a variant) corresponding to 8-18 of AAW14499 is deleted
FT		or replaced with a fragment corresponding to this
FT		fragment; claim 35"
FT	Misc-difference	28. .42
FT		/label= loop 1 modification region
FT		/note= "at least one amino acid residue of a parent alpha
FT		-amylase (used as a template for a variant) corresponding
FT		to 12-19 of AAW14499 is deleted or replaced with a
FT		fragment corresponding to this fragment; claim 30"
FT	Misc-difference	32. .38
FT		/label= loop 1 modification region
FT		/note= "preferred region where at least one amino acid
FT		residue of a parent alpha-amylase (used as a template for
FT		a variant) corresponding to 14-15 of AAW14499 is deleted
FT		or replaced with a fragment corresponding to this
FT		fragment; claim 32"
FT	Misc-difference	66. .84
FT		/label= loop 2 modification region
FT		/note= "at least one amino acid residue of a parent alpha
FT		-amylase (used as a template for a variant) corresponding
FT		to 44-57 of AAW14499 is deleted or replaced with a
FT		fragment corresponding to this fragment; claim 18"
FT	Misc-difference	70. .78
FT		/label= loop 2 modification region
FT		/note= "preferred region where at least one amino acid
FT		residue of a parent alpha-amylase (used as a template for
FT		a variant) corresponding to 48-51 of AAW14499 is deleted
FT		or replaced with a fragment corresponding to this
FT		fragment; claim 20"
FT	Misc-difference	98. .210
FT		/label= loop 3 modification region
FT		/note= "at least one amino acid residue of a parent alpha
FT		-amylase (used as a template for a variant) corresponding
FT		to 117-185 of AAW14499 is deleted or replaced with a
FT		fragment corresponding to this fragment; claim 24"
FT	Misc-difference	102. .206
FT		/label= loop 3 modification region
FT		/note= "preferred region where at least one amino acid
FT		residue of a parent alpha-amylase (used as a template for
FT		a variant) corresponding to 121-181 of AAW14499 is
FT		deleted or replaced with a fragment corresponding to this
FT		fragment; claim 26"
FT	Misc-difference	121. .181
FT		/note= "at least one amino acid residue of a parent alpha
FT		-amylase (used as a template for a variant) corresponding
FT		to this fragment is deleted or replaced with a fragment
FT		corresponding to 102-206 of AAW14499; claim 41"
FT	Misc-difference	121. .174
FT		/note= "preferred region where at least one amino acid
FT		residue of a parent alpha-amylase (used as a template for
FT		a variant) corresponding to this fragment is deleted or
FT		replaced with a fragment corresponding to 102-199 of
FT		AAW14499; claim 42"
FT	Misc-difference	165. .177
FT		/label= loop 3 modification region
FT		/note= "at least one amino acid residue of a parent alpha
FT		-amylase (used as a template for a variant) corresponding
FT		to 195-202 of AAW14499 is deleted or replaced with a
FT		fragment corresponding to this fragment; claim 21"
FT	Misc-difference	166. .173
FT		/label= loop 3 modification region
FT		/note= "preferred region where at least one amino acid
FT		residue of a parent alpha-amylase (used as a template for
FT		a variant) corresponding to this fragment is deleted or
FT		replaced with a fragment corresponding to 102-199 of
FT		AAW14499; claim 42"

FT		residue of a parent alpha-amylase (used as a template for a variant) corresponding to 196-198 of AAW14499 is deleted or replaced with a fragment corresponding to this fragment; claim 23"
FT	Misc-difference	181..184
FT		/note= "an amino acid fragment corresponding to this region is deleted from the parent sequence of a variant Fungamyl; claim 43"
FT	Misc-difference	291..313
FT		/label= loop 8 modification region
FT		-/note= "at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 322-346 of AAW1498 is deleted or replaced with a fragment corresponding to this fragment; claim 36"
FT	Misc-difference	297..313
FT		/label= loop 8 modification region
FT		-/note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 325-345 of AAW14498 is deleted or replaced with a fragment corresponding to this fragment; claim 38"
XX		
PN	WO9223874-A1.	
XX		
PD	08-AUG-1996.	
XX		
PF	05-FEB-1996;	96WO-DK000057.
XX		
PR	03-FEB-1995;	95DK-00000128.
PR	23-OCT-1995;	95DK-00001192.
PR	10-NOV-1995;	95DK-00001256.
XX		
PA	(NOVO) NOVO-NORDISK AS.	
XX		
PI	Svendsen A, Bisgard-Prantzen H, Borchert TV;	
XX		
DR	WPI; 1996-371424/37.	
XX		
PT	Alpha-amylase variants and methods of production - have altered properties such as calcium dependency, substrate binding and stability.	
PS	Disclosure; Page 87-88; 17lpp; English.	
XX		
CC	The present sequence is the mature Aspergillus oryzae alpha-amylase (A).	
CC	Variants of parent termamyl- and fungamyl-like alpha-amylases (and methods of constructing them) are claimed. Examples of variants are featured above. The variants have altered properties such as calcium dependency, substrate binding and stability. Also one or more proline or cysteine residues in the variant is modified or replaced with a non-proline or non-cysteine residue such as alanine. The variants can be used for (dish)washing, as detergent additives or for fabric desizing or starch liquefaction. They can also be used for the production of CC sweeteners and ethanol from starch. See also AAW14498-99	
XX		
SQ	Sequence 478 AA;	
	Query Match	100.0%; Score 13; DB 2; Length 478;
	Best Local Similarity	100.0%; Pred.No. 2e-06;
	Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Qy	1 AYHGYWQQDIYSL 13	
Dd	78 AYHGYWQQDIYSL 90	
RESULT 5		
AAB84206	ID	AAB84206 standard; protein; 498 AA.
XX	AC	AAB84206;
XX	DT	06-AUG-2001 (first entry)
XX		

CC The sequences given in ABB90164-87 show enzymatic proteins derived from
CC *A. fumigatus*. These proteins display the catalytic activity of an enzyme
CC such as tannase, cellulase, glucose oxidase, glucoamylase, phytase, beta-
CC galactosidases, invertase, lipase, alpha-amylase, laccase,
CC polygalacturonase or xylanase. Compositions comprising the tannase are
CC useful for modulating the amount of compounds that comprise a gallate
CC ester linkage in a composition. Compositions comprising cellulase are
CC useful for modulating the amount of cellulose in a composition.
CC Compositions comprising glucose oxidase are useful for modulating the
CC amount of glucose or oxygen in a composition. Compositions comprising
CC phytase are useful for modulating the amount of myo-inositol phosphates
CC in a composition. Compositions comprising beta-galactosidases are useful
CC for modulating the amount of lactose in a composition. Compositions
CC comprising sucrose or invertase are useful for modulating the amount of
CC sucrose in a composition. Compositions comprising lipase are useful for

modulating the amount of glyceride in a composition. Compositions comprising alpha-amylases are useful for modulating the amount of starches or maltodextrins in a composition. Compositions comprising laccase are useful for modulating the amount of oxidated phenolic compounds in a composition. Compositions comprising polygalacturonases are useful for modulating the amount of high or low molecular weight polygalacturonic acid chains in a composition. Compositions comprising xylanases are useful for modulating the amount of xylan or xylo-oligomers in a composition. The A. fumigatus proteins and corresponding DNA's are useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents. The DNA's are useful to express recombinant enzymes for characterization, modification or industrial uses, to compare with the nucleotide sequence of A. fumigatus to identify duplicated genes of paralogs having the same or similar biochemical activity and/or function, to compare with nucleic acid sequence of other related or distant fungal organisms to identify potential orthologous enzyme genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, and to raise anti-protein antibodies. The polypeptide having tannase activity increases the yield of tea liquor from tea leaves, improves the colour, flavour and health benefits of tea products, particularly an instant tea product. The polypeptide having cellulase activity enhances cleaning ability of detergent compositions

XX SQ Sequence 495 AA;

Query Match 92.3%; Score 12; DB 6; Length 495;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGWWQDIYS 12
| | | | | | | | | |
DB 97 AYHGWWQDIYS 108

RESULT 10
ABB09072
ID ABB09072 standard; protein; 423 AA.
XX
AC ABB09072;
XX
DT 26-JUN-2002 (first entry)
XX
DE Aspergillus oryzae TAKA protein (TAA).
XX
KW Thermus sp. IM6501; maltogenic amylase; EC 3.2.1.133; crystallisation;
KW protein co-ordinate data; 3 dimensional structure.
XX
OS Aspergillus oryzae.
XX
PN KR2001027418-A.
XX
PD 06-APR-2001.
XX
PF 09-SEP-1999; 99KR-00039130.
XX
PR 09-SEP-1999; 99KR-00039130.
XX
PA (POST-) POSTECH FOUND.
PA (SAMY-) SAMYANG GENEX CORP.
XX
PI Kim TJ, Park GH;
XX
DR WPI; 2001-534477/59.

Manufacturing maltogenic amylase having improved transglycosylation activity, comprises using crystallization.
XX
PS Disclosure; Page 188; 196pp; Korean.
XX
CC The present invention describes manufacturing maltogenic amylase (EC 3.2.1.133) having improved transglycosylation activity, comprising using crystallisation and the three dimensional structure of maltogenic

amylase. Manufacturing maltogenic amylase comprises the following steps:
CC (i) obtaining a gene of maltogenic amylase from *Thermus* sp. IM6501 (KCTC 5027BP) and inserting the gene into plasmid pUC119 to construct
CC recombinant DNA (pTNA119); (ii) inserting the recombinant DNA to
CC *Escherichia coli* MC1061, which is cultivated at 37 plus degrees Celsius
CC for 10 hours in Luria-Bertani (LB) media and centrifuging the media to
CC obtain a microbial cell; (iii) suspending the microbial cell with buffer
CC solution at pH 7.5 and obtaining supernatant; and (iv) passing the
CC supernatant through column chromatography and obtaining purified
CC maltogenic amylase. The maltogenic amylase is a dimer comprised of two
CC maltogenic amylase molecules, and a *Thermus* sp. IM6501 maltogenic amylase
CC (TMA) crystal. The amylase has a structure containing an activated
CC region that consists of amino acid residues of Asp-328, Glu-357, Asp-424,
CC and a pocket with glucose bound that consists of amino acid residues of
CC Pro44, Tyr45, Arg81, Arg83, Prol18, Cys116, Asn131, Glu132, Val1329,
CC and His1360. The present sequence represents *Aspergillus oryzae* TAKA
CC protein (TAA), given in comparison with TMA in the present invention
XX SQ Sequence 423 AA;

Query Match 84.6%; Score 11; DB 4; Length 423;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HGYWQDIYSL 13
| | | | | | | | | |
DB 76 HGYWQDIYSL 86

RESULT 11
ABP97894
ID ABP97894 standard; protein; 494 AA.
XX
AC ABP97894;
XX
DT 17-JUN-2003 (first entry)
XX
DE Amino acid sequence of an alpha-amylase of *Aspergillus niger*.
XX
KW Alpha-amylase; enzyme; endohydrolysis; 1,4-alpha-glucosidic linkage;
KW oligosaccharide; polysaccharide; baking.
XX
OS Aspergillus niger.
XX
PN WO2003016535-A2.
XX
PD 27-FEB-2003.
XX
PF 02-AUG-2002; 2002WO-NL000522.
XX
PR 16-AUG-2001; 2001EP-00000379.
PR 16-AUG-2001; 2001EP-00000380.
PR 16-AUG-2001; 2001EP-00000381.
PR 16-AUG-2001; 2001EP-00000382.
PR 16-AUG-2001; 2001EP-00000383.
PR 16-AUG-2001; 2001EP-00000384.
XX
PA (STAM) DSM NV.
XX
PI Maier D, Stock A, Wagner C, Folkers U, Albermann K, Hopper S;
XX
DR WPI; 2003-312758/30.
XX
PT New polynucleotide from a filamentous fungus, preferably *Aspergillus niger*, useful in a baking process.
XX
PS Claim 13; Page 61-63; 81pp; English.
XX
CC The present sequence is an alpha-amylase enzyme of the filamentous fungus
CC *Aspergillus niger*. Alpha-amylases catalyse the endohydrolysis of 1,4-
CC alpha-glucosidic linkages in oligosaccharides and polysaccharides. The
CC alpha-amylase polynucleotides and polypeptides of the invention are
CC useful in a baking process

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XX SQ Sequence 494 AA;
Query Match 69.2%; Score 9; DB 6; Length 494;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQD 9
    |||||
DB 94 AYHGYWQD 102

RESULT 12
ID AAE24207 standard; protein; 484 AA.
XX AAE24207;
AC AAE24207;
XX 04-OCT-2002 (first entry)
XX Aspergillus niger alpha-amylase protein.
XX Ethanol production; starch; fermentation; liquefaction; alpha-amylase;
KW fuel alcohol; fuel additive; neutral spirit; industrial ethanol; enzyme.
XX Aspergillus niger.
OS WO200238787-A2.
XX 16-MAY-2002.
XX 09-NOV-2001; 2001WO-DK000737.
XX 10-NOV-2000; 2000DK-00001676.
PR 21-NOV-2000; 2000US-0252213P.
PR 11-DEC-2000; 2000DK-00001854.
PR 15-DEC-2000; 2000US-0256015P.
XX (NOVO ) NOVOZYMES AS.
PA (NOVO ) NOVOZYMES NORTH AMERICA INC.
XX Veit C, Felby C, Fuglsang CC;
XX WPI; 2002-479793/51.
XX Producing ethanol from starch-containing material e.g., tubers, roots,
PT whole grain, for use in fuel, by fermentation comprises carrying out a
PT secondary liquefaction step in the presence of a thermostable acid alpha-
PT amylase.
XX Claim 35; Page 31-33; 33pp; English.
XX The invention relates to a method for producing ethanol from starch-
CC containing material, by fermentation. The method involves carrying out a
CC secondary liquefaction step in the presence of a thermostable acid alpha-
CC amylase. The method is used in producing ethanol from a starch-containing
CC material such as tubers, roots or whole grain (e.g. corn, wheat or barley
CC or their combination) or combination of the materials. Preferably ethanol
CC is produced from starch-containing material that is obtained from cereals
CC or from corns, cobs, wheat, barley, rye, milo and potatoes or their
CC combination. The ethanol produced by above mentioned method is used as
CC fuel alcohol and/or fuel additive. The ethanol is also useful as drinking
CC ethanol i.e., potable neutral spirits or industrial ethanol. The present
CC sequence is Aspergillus niger alpha-amylase protein
XX Sequence 484 AA;
Query Match 61.5%; Score 8; DB 5; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQ 8
    |||||
DB 78 AYHGYWQ 85

RESULT 14
ABB80178
ID ABB80178 standard; protein; 630 AA.
XX ABB80178;
AC ABB80178;
XX 11-AUG-2003 (first entry)
DT A. fumigatus AFAAL2.
DE Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
XX beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
KW

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DB 78 AYHGYWQ 85

RESULT 13
ADS75939
ID ADS75939 standard; protein; 484 AA.
XX ADS75939;
AC ADS75939;
XX 16-DEC-2004 (first entry)
DT Aspergillus niger acid alpha-amylase for ethanol production method.
XX Aspergillus niger.
OS WO2004080923-A2.
XX 23-SEP-2004.
XX 10-MAR-2004; 2004WO-DK000154.
PF 10-MAR-2003; 2003US-0453326P.
XX (NOVO ) NOVOZYMES AS.
XX Olsen HS, Pedersen S, Festeren RM;
PI WPI; 2004-677503/66.
DR Production of alcohol product, e.g. beer, comprises holding slurry of
XX water and granular starch in presence of acid alpha-amylase and
XX glucoamylase followed by simultaneous saccharification and fermentation.
XX Claim 9; SEQ ID NO 1; 43pp; English.
XX The invention relates to a method for the production of an alcohol
CC product by holding a slurry of water and granular starch in the presence
CC of an acid alpha-amylase and a glucoamylase at 0-20 deg C below the
CC initial gelatinization temperature of the granular starch; holding the
CC slurry in the presence of acid alpha-amylase, glucoamylase and yeast at
CC 10-35 deg C to produce ethanol; and optionally recovering the ethanol.
CC The method is used for the production of an alcohol product such as beer
CC or recovered ethanol, e.g. fuel ethanol, potable ethanol or industrial
CC ethanol. This sequence represents an acid fungal alpha-amylase from
CC Aspergillus niger used in the method of the invention.
XX Sequence 484 AA;
Query Match 61.5%; Score 8; DB 8; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQ 8
    |||||
DB 78 AYHGYWQ 85

RESULT 14
ABB80178
ID ABB80178 standard; protein; 630 AA.
XX ABB80178;
AC ABB80178;
XX 11-AUG-2003 (first entry)
DT A. fumigatus AFAAL2.
DE Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
XX beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
KW

```

KW polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
KW glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
KW glyceride; starch; maltodextrin; oxidized phenolic compound;
KW polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
KW textile; tea liquor; cleaning ability.

XX Aspergillus fumigatus.

OS
XX WO2003012071-A2.

XX
XX 13-FEB-2003.

XX
XX 05-AUG-2002; 2002WO-US024842.

XX
XX 03-AUG-2001; 2001US-0309870P.

XX (ELIT-) ELITRA PHARM INC.

XX Jiang B, Storms R, Roemer T, Bussey H;

XX WPI; 2003-332729/31.

XX N-PSDB; ABQ80347, ABQ80348.

XX Novel isolated Aspergillus fumigatus polypeptide, useful in various
PT industries such as those involved in the making of food and feed,
PT beverages, textiles and detergents.

XX Claim 17; Page 139-40; 169pp; English.

XX The sequences given in ABB80164-87 show enzymatic proteins derived from
CC A. fumigatus. These proteins display the catalytic activity of an enzyme
CC such as tannase, cellulase, glucose oxidase, glucoamylase, phytase, beta-
CC galactosidases, invertase, lipase, alpha-amylase, lactase, beta-
CC polygalacturonase or xylanase. Compositions comprising the tannase are
CC useful for modulating the amount of compounds that comprise a gallate
CC ester linkage in a composition. Compositions comprising cellulase are
CC useful for modulating the amount of cellulose in a composition.

CC Compositions comprising glucose oxidase are useful for modulating the
CC amount of glucose or oxygen in a composition. Compositions comprising
CC phytase are useful for modulating the amount of myo-inositol phosphates
CC in a composition. Compositions comprising beta-galactosidases are useful
CC for modulating the amount of lactose in a composition. Compositions
CC comprising sucrose or invertase are useful for modulating the amount of
CC sucrose in a composition. Compositions comprising lipase are useful for
CC modulating the amount of glyceride in a composition. Compositions
CC comprising alpha-amylases are useful for modulating the amount of
CC starches or maltodextrins in a composition. Compositions comprising
CC lactase are useful for modulating the amount of oxidized phenolic
CC compounds in a composition. Compositions comprising polygalacturonases
CC are useful for modulating the amount of high or low molecular weight
CC polygalacturonic acid chains in a composition. Compositions comprising
CC xylanases are useful for modulating the amount of xylan or xylo-oligomers
CC in a composition. The A. fumigatus proteins and corresponding DNA's are
CC useful in various industries such as those involved in the making of food
CC and feed, beverages, textiles and detergents. The DNA's are useful to
CC express recombinant enzymes for characterization, modification or
CC industrial uses, to compare with the nucleotide sequence of A. fumigatus
CC to identify duplicated genes of paralogs having the same or similar
CC biochemical activity and/or function, to compare with nucleic acid
CC sequence of other related or distant fungal organisms to identify
CC potential orthologous enzyme genes, for selecting and making oligomers
CC for attachment to a nucleic acid array for examination of expression
CC patterns, and to raise anti-protein antibodies. The polypeptide having
CC tannase activity increases the yield of tea liquor from tea leaves,
CC improves the colour, flavour and health benefits of tea products,
CC particularly an instant tea product. The polypeptide having cellulase
CC activity enhances cleaning ability of detergent compositions

XX Sequence 630 AA;

Query Match 53.8%; Score 7; DB 6; Length 630;

Best Local Similarity 100.0%; Pred. No. 9.9;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YHGYWQQ 8
| | | | |
Db 102 YHGYWQQ 108

RESULT 15

AAR85808
ID AAR85808 standard; peptide; 31 AA.

XX
AC AAR85808;

XX
DT 13-SEP-1996 (first entry)

XX Peptide rII from the WD-40 domain-contg. TUP1 protein.

XX WD40 repeat region; beta-transducin; protein-protein interaction; drug;
KW intracellular signalling; protein kinase C; homology; motif; modulator;
KW receptors of activated protein kinase; enzyme activity; isozyme; human.

XX Synthetic.

XX WO9521252-A2.

XX 10-AUG-1995.

XX 31-JAN-1995; 95WO-US001210.

XX 01-FEB-1994; 94US-00190802.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D, Ron D;

XX WPI; 1995-283772/37.

XX New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the
PT activity of a protein, eg. protein kinase C, which interacts with a
PT protein contg. a WD-40 region.

XX Claim 3; Page 271; 351pp; English.

XX The peptides AAR84928-R85063 and AAR85786-R85842 are peptides derived
CC from the WD40 regions of a range of proteins (AAR85851-R85893) containing
CC WD-40 (also called beta-transducin) amino acid repeat regions. The WD-40
CC regions are involved in protein-protein interactions between proteins
CC involved in intracellular signalling. An example of such an interaction
CC is between protein kinase C and receptors of activated protein kinase
CC (RACK), esp. RACK-1 (AAR85850). The proteins were isolated based on
CC homology with beta-transducin or with its WD-40 consensus sequence. The
CC peptides can be used to identify target proteins contg. WD-40 motifs, as
CC modulators of enzyme esp. isozyme, activity of proteins involved in
CC protein-protein interaction and to screen for drugs that will affect
CC protein-protein interaction involving WD-40 domains. This peptide is
CC derived from the repeat II from the TUP1 protein

XX Sequence 31 AA;

Query Match 46.2%; Score 6; DB 2; Length 31;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QDIYSL 13
| | | | |

Db 4 QDIYSL 9

Search completed: November 7, 2005, 19:27:55

Job time : 8.47876 secs

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OM protein - protein search, using sw model

Run on: November 7, 2005, 19:15:40 ; Search time 1.58108 Seconds
(without alignments)
791.116 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110
Perfect score: 13
Sequence: 1 AVHGYWQDIYSL 13

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 79.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	100.0	498	2 A48305	alpha-amylase (EC
2	13	100.0	499	1 ALAS1	alpha-amylase (EC
3	13	100.0	499	1 ALAS3	alpha-amylase (EC
4	13	100.0	499	2 JS0663	alpha-amylase (EC
5	13	100.0	499	2 JT0466	alpha-amylase (EC
6	13	100.0	499	2 JN0588	alpha-amylase (EC
7	13	100.0	499	2 B48305	alpha-amylase (EC
8	8	61.5	484	1 A35282	alpha-amylase (EC
9	6	46.2	429	2 T41560	phenylalanyl-trna
10	6	46.2	478	2 T40860	probable alpha-am
11	6	46.2	482	2 S31478	alpha-amylase (EC
12	6	46.2	483	2 G75392	glycosyl hydrolase
13	6	46.2	491	2 T38448	probable alpha-am
14	6	46.2	494	1 ALBYAF	alpha-amylase (EC
15	6	46.2	507	2 S33921	alpha-amylase (EC
16	6	46.2	512	2 S23355	alpha-amylase (EC
17	6	46.2	512	2 S06115	alpha-amylase (EC
18	6	46.2	513	2 T38770	alpha-amylase a pr
19	6	46.2	528	1 ALBSK	alpha-amylase (EC
20	6	46.2	564	2 T41503	alpha-amylase - fi
21	6	46.2	614	2 S58306	WD-40 repeat regul
22	6	46.2	624	1 JC4510	pullulanase (EC 3
23	6	46.2	625	2 T41603	alpha-amylase - fi
24	6	46.2	631	2 S72270	alpha-amylase (EC
25	6	46.2	690	2 B82409	alpha-amylase VCAO
26	6	46.2	712	1 ALBSG3	cyclomaltodextrin
27	6	46.2	713	1 ALBSG7	cyclomaltodextrin
28	6	46.2	713	1 ALBSG1	cyclomaltodextrin
29	6	46.2	713	1 ALBSR4	cyclomaltodextrin

30	6	46.2	713	2 A58800	cyclomaltodextrin
31	6	46.2	713	2 S09196	cyclomaltodextrin
32	6	46.2	713	2 JN0133	WD-40 repeat regul
33	6	46.2	718	1 ALBSG6	cyclomaltodextrin
34	6	46.2	718	1 ALBSGC	cyclomaltodextrin
35	6	46.2	718	1 ALBSMX	cyclomaltodextrin
36	5	38.5	20	2 S50175	kallikrein (PK-120
37	5	38.5	87	2 B95193	yimG protein (Impo
38	5	38.5	87	2 B99060	conserved hypotet
39	5	38.5	103	2 AF1183	hypothetical prote
40	5	38.5	103	2 AG1540	hypothetical prote
41	5	38.5	189	2 P97007	xanthine phosphori
42	5	38.5	204	2 AF1237	SOS response regul
43	5	38.5	204	2 AC1600	SOS response regul
44	5	38.5	218	2 B86801	prophage p13 prote
45	5	38.5	227	2 P96955	ABC-transporter, A

ALIGNMENTS

RESULT 1

A48305
alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori
C;Species: Aspergillus awamori
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: A48305
R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe
A;Reference number: A48305; MUID:90254827; PMID:2340591
A;Accession: A48305
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA

A;Residues: 1-498 <KOR>

A;Cross-references: UNIPROT:Q02905

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation

C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F;194-321/Domain: alpha-amylase core homology <AMY>

Query Match 100.0%; Score 13; DB 2; Length 498;

Best Local Similarity 100.0%; Pred. No. 3.2e-08;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVHGYWQDIYSL 13

Db 99 AVHGYWQDIYSL 111

RESULT 2

ALAS1

alpha-amylase (EC 3.2.1.1) 1 precursor [validated] - Aspergillus oryzae

N;Alternate names: alpha-amylase isozyme II; glycogenase; Taka-amylase A

C;Species: Aspergillus oryzae

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C;Accession: S04548; A33214; J50240; A91930; A93767; A10627

R;Wiesel, S.; Lachmund, A.; Wildhardt, G.; Rutkowski, E.

Mol. Microbiol. 3, 3-14, 1989

A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon
A;Reference number: S04548; MUID:89237897; PMID:2785629

A;Accession: S04548

A;Molecule type: DNA

A;Residues: 1-499 <WIR>

A;Cross-references: UNIPROT:P10529; EMBL:X12725; NID:G2430; PIDN:CAA31218.1; PID:G29592

A;Genetics: AMY1

A;Accession: A33214

A;Molecule type: mRNA

A;Residues: 1-499 <W12>

A;Cross-references: GB:X12725; NID:G2430; PIDN:CAA31218.1; PID:G295921

R;Genes, M.J.; Dove, M.J.; Seligy, V.L.

A;Accession: A33215
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-499 <WT2>
A;Cross-references: GB:X12727; NID:G2454; PIDN:CAA31220.1; PID:g295922
R;Genes, M.J.; Dove, M.J.; Seligy, V.I.
Gene 79, 107-117, 1989
A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containin
A;Reference number: JS0240; MUID:89378767; PMID:2789162
A;Accession: A44713
A;Molecule type: DNA
A;Residues: 1-499 <GEN>
A;Note: the authors refer to this as isozyme I
R;Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
A;Title: Structure and possible catalytic residues of Taka-amylase A.
A;Reference number: A37454; MUID:84212370; PMID:6609921
A;Contents: annotation; X-ray crystallography, 3.0 angstroms
C;Comment: One atom of calcium per molecule is essential for activity.
C;Genetics:
A;Gene: amy3; AmyI
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; meta
F;1-21/Domain: signal sequence #status predicted <SIG>
F;12-499/Product: alpha-amylase 3 #status experimental <MAT>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;51-59,171-183,261-304,461-496/Disulfide bonds: #status experimental
F;142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;231,251,318/Active site: His, Glu, Asp #status experimental

Query Match 100.0%; Score 13; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDDIYSL 13
| | | | | | | | | | | | | | | | | | | | | |
Db 99 AYHGYYQDDIYSL 111

RESULT 4
JS0663
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus sp.
C;Species: Aspergillus sp.
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
C;Accession: JS0663
R;Shibuya, I.; Tamura, G.; Ishikawa, T.; Hara, S.
Biosci. Biotechnol. Biochem. 56, 174-179, 1992
A;Title: Cloning of the alpha-amylase cDNA of Aspergillus shiroyamii and its expressio
A;Reference number: JS0663; MUID:92323146; PMID:1368777
A;Accession: JS0663
A;Molecule type: mRNA
A;Residues: 1-499 <SHI>
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;12-499/Product: alpha-amylase #status predicted <ALP>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 13; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDDIYSL 13
| | | | | | | | | | | | | | | | | | | | | |

Db 99 AYHGYWQDIYSL 111

RESULT 5

JT0466
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N;Alternate names: glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: JT0466
R;Tada, S.; Iimura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.
Agric. Biol. Chem. 53, 593-599, 1989
A;Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergillus oryzae
A;Reference number: JT0466
A;Accession: JT0466
A;Molecule type: DNA
A;Residues: 1-499 <TAD>
A;Cross-references: UNIPROT:P10529
C;Comment: See also PIR:JK0201 and PIR:JS0240.
C;Comment: One atom of calcium per molecule is essential for activity.
C;Genetics:
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase #status predicted <MAT>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;231,251,318/Active site: His, Glu, Asp #status predicted

Query Match 100.0%; Score 13; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
|||||
Db 99 AYHGYWQDIYSL 111

RESULT 6

JN0588
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N;Alternate names: Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: JN0588
R;Tsukagoshi, N.; Furukawa, M.; Nagaba, H.; Kiritu, N.; Tsuboi, A.; Udaka, S.
Gene 84, 319-327, 1989
A;Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for multiple forms of the enzyme
A;Reference number: JN0588; MUID:90128276; PMID:2612911
A;Accession: JN0588
A;Molecule type: mRNA
A;Residues: 1-499 <TSU>
A;Cross-references: UNIPROT:Q96TH4
C;Comment: The alpha amylases are encoded by multigene family.
C;Genetics:

A;Gene: Taa-GI
A;Introns: 56/1; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase #status predicted <MAT>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 13; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AYHGYWQDIYSL 13
|||||
Db 99 AYHGYWQDIYSL 111

RESULT 7

B48305
alpha-amylase (EC 3.2.1.1) B precursor - Aspergillus awamori
C;Species: Aspergillus awamori
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: B48305
R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.; Curr. Genet. 17, 203-212, 1990
A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspergillus awamori
A;Reference number: A48305; MUID:90254827; PMID:2340591
A;Accession: B48305
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-499 <KOR>
A;Cross-references: UNIPROT:Q02906
C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology <AMY>

Query Match 100.0%; Score 13; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
|||||
Db 99 AYHGYWQDIYSL 111

RESULT 8

A35282
alpha-amylase (EC 3.2.1.1) - Aspergillus niger
C;Species: Aspergillus niger
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A35282
R;Boel, E.; Brady, L.; Brzozowski, A.M.; Derewenda, Z.; Dodson, G.G.; Jensen, V.J.; Pet. Biochemistry 29, 6244-6249, 1990
A;Title: Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-angstrom
A;Reference number: A35282; MUID:91002514; PMID:2207069
A;Accession: A35282
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr

A;Molecule type: mRNA
A;Residues: 1-484 <BOE>
C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;173-300/Domain: alpha-amylase core homology <AMY>

Query Match 61.5%; Score 8; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQ 8
|||||
Db 78 AYHGYWQ 85

RESULT 9

T41560
phenylalanyl-trna synthetase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T41560
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z21991
A;Accession: T41560
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-429 <WOO>
A;Cross-references: UNIPROT:O74952; EMBL:AL023705; GSPDB:GN00068; SPDB:
A;Experimental source: strain 972h-; cosmid c736
C;Genetics:
A;Gene: SPDB:SPCC736.03c
A;Map position: 3
C;Superfamily: phenylalanine-tRNA ligase alpha chain

Query Match 46.2%; Score 6; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QDIYSL 13
Db 203 QDIYSL 208

RESULT 10
T40860
probable alpha-amylase precursor SPCC11E10.09c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40860; T41181
R;Rampersger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z21952
A;Accession: T40860
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-478 <RAM>
A;Cross-references: UNIPROT:Q10427; EMBL:AL121783; NID:G6016988; PIDN:CAB57851.1; PID:96
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.
submitted to the EMBL Data Library, April 1999
A;Reference number: Z21976
A;Accession: T41181
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-203 <LYN>
A;Cross-references: EMBL:AL049662; NID:G4678680; PIDN:CAB41221.1; PID:G4678681; GSPDB:GN
A;Experimental source: strain 972h-; cosmid c188
C;Genetics:
A;Gene: SPDB:SPCC11E10.09c; SPDB:SPCC188.01c
A;Map position: 3
A;Introns: 320/3; 468/3
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

Query Match 46.2%; Score 6; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYW 6
Db 89 AYHGYW 94

RESULT 11
S31478
alpha-amylase (EC 3.2.1.1) - Thermoactinomyces vulgaris
C;Species: Thermoactinomyces vulgaris
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S31478
R;Hofemeister, B.; Koenig, S.; Hoang, V.; Engel, J.; Mayer, G.; Heese, O.; Hansen, G.; H
submitted to the EMBL Data Library, December 1992
A;Description: The gene amyTV coding for a non-glucogenic alpha-amylase from Thermoactin
A;Reference number: S31478

A;Accession: S31478
A;Molecule type: DNA
A;Residues: 1-482 <HOF>
A;Cross-references: UNIPROT:Q60051; EMBL:X69807; NID:G48289; PIDN:CAA49465.1; PID:G4829
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;194-319/Domain: alpha-amylase core homology <AMY>

Query Match 46.2%; Score 6; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYW 6
Db 107 AYHGYW 112

RESULT 12
G75392
glycosyl hydrolase, family 13 - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: G75392
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75392
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-483 <WHI>
A;Cross-references: UNIPROT:O9RU88; GB:AE001991; GB:AE000513; NID:G6459223; PIDN:AAF110
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1472
A;Map position: 1
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

Query Match 46.2%; Score 6; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYW 6
Db 101 AYHGYW 106

RESULT 13
T38448
probable alpha-amylase precursor - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38448
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21749
A;Accession: T38448
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-491 <MUR>
A;Cross-references: UNIPROT:O13996; EMBL:Z98978; PIDN:CAB11675.1; GSPDB:GN00066; SPDB:S
A;Experimental source: strain 972h-; cosmid c27E2
C;Genetics:
A;Gene: SPDB:SPAC27E2.01
A;Map position: 1
A;Introns: 325/3; 476/3
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

Query Match 46.2%; Score 6; DB 2; Length 491;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYW 6
| | | | |
DB 94 AYHGYW 99

RESULT 14
ALBYAF
alpha-amylase (EC 3.2.1.1) precursor - yeast (Saccharomycopsis fibuligera)
C;Species: Saccharomycopsis fibuligera
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: S00064
R;Itoh, T.; Yamashita, I.; Fukui, S.
FEBS Lett. 219, 339-342, 1987
A;Title: Nucleotide sequence of the alpha-amylase gene (ALP1) in the yeast Saccharomycop
A;Reference number: S00064; MUID:87276512; PMID:3497057
A;Accession: S00064
A;Molecule type: DNA
A;Residues: 1-494 <ITO>
A;Cross-references: UNIPROT:P21567; EMBL:X05791; NID:94847; PIDN:CAA29233.1; PID:94848
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in having 368-Thr
C;Genetics:
A;Gene: ALP1
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: calcium; extracellular protein; glycoprotein; glycosidase; hydrolase; metallo
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-494/Product: alpha-amylase #status predicted <MAT>
F;200-327/Domain: alpha-amylase core homology <AMY>
F;57-65,177-191,267-310,462-493/Disulfide bonds: #status predicted
F;148,189,202,237/Binding site: calcium (Asn, Gln, Asp, His) #status predicted
F;224/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;233,257,324/Active site: Asp, Glu, Asp #status predicted

Query Match 46.2%; Score 6; DB 1; Length 494;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYW 6
| | | | |
DB 105 AYHGYW 110

RESULT 15
S33921
alpha-amylase (EC 3.2.1.1) SWA2 precursor - yeast (Schwanniomyces occidentalis)
N;Alternate names: alpha-1,4 glucanohydrolase
C;Species: Schwanniomyces occidentalis
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S33921
R;Claros, M.G.; Abarca, D.; Fernandez-Lobato, M.; Jimenez, A.
Curr. Genet. 24, 75-83, 1993
A;Title: Molecular structure of the SWA2 gene encoding an AMY1-related alpha-amylase fro
A;Reference number: S33921; MUID:93365041; PMID:8358835
A;Accession: S33921
A;Molecule type: DNA
A;Residues: 1-507 <CLA>
A;Cross-references: UNIPROT:Q08806; EMBL:X73497; NID:g396561; PIDN:CAA51912.1; PID:g3965
C;Genetics:
A;Gene: SWA2
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-507/Product: alpha-amylase #status predicted <MAT>
F;205-332/Domain: alpha-amylase core homology <AMY>

F;134,229/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 46.2%; Score 6; DB 2; Length 507;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYW 6
| | | | |
DB 110 AYHGYW 115

Search completed: November 7, 2005, 19:33:47
Job time : 1.58108 secs

It's Pigeon Blue (1991)

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OM protein - protein search, using sw model

Run on: November 7, 2005, 19:00:20 ; Search time 6.90154 Seconds
(without alignments)
964.571 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110
Perfect score: 13
Sequence: 1 AHHGYWQQDIYSL 13

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UniProt 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	498	1 AMYA ASPAW	Q02905 aspergillus
2	13	100.0	498	2 Q76CT3	Q76CT3 aspergillus
3	13	100.0	499	1 AMYA ASPOR	P10529 aspergillus
4	13	100.0	499	1 AMYA ASPAW	Q02906 aspergillus
5	13	100.0	499	1 AMYA ASPSH	P30292 aspergillus
6	13	100.0	499	2 Q96TH4	Q96TH4 aspergillus
7	13	100.0	499	2 Q76L99	Q76L99 aspergillus
8	13	100.0	499	2 Q7LV45	Q7LV45 aspergillus
9	11	84.6	490	2 Q9UV07	Q9UV07 emericella
10	10	76.9	128	2 O15751	O15751 dictyosteli
11	8	61.5	484	1 AMYA ASPNG	P56271 aspergillus
12	8	61.5	634	2 Q76L96	Q76L96 aspergillus
13	8	61.5	640	2 O13296	O13296 aspergillus
14	6	46.2	322	2 Q6Y198	Q6Y198 picchia angu
15	6	46.2	413	2 Q9MER9	Q9MER9 malus domes
16	6	46.2	415	2 Q6CDK9	Q6CDK9 yarrowia li
17	6	46.2	429	2 Q74952	Q74952 schizosacch
18	6	46.2	478	1 YQ29 SCHPO	O10427 schizosacch
19	6	46.2	482	2 Q60051	Q60051 thermoactin
20	6	46.2	483	2 Q9RUB8	Q9RUB8 deinococcus
21	6	46.2	491	2 O13996	O13996 schizosacch
22	6	46.2	494	1 AMY1 SACFI	P21567 saccharomyc
23	6	46.2	503	2 Q8RIQ6	Q8RIQ6 fusobacteri
24	6	46.2	507	1 AMY2 DEBOC	Q08806 debaryomyce
25	6	46.2	512	1 AMY1 DEBOC	P19269 debaryomyce
26	6	46.2	512	2 Q7P5Z5	Q7P5Z5 fusobacteri
27	6	46.2	513	1 AMY3 SCHPO	O14154 schizosacch
28	6	46.2	514	1 TUP1 CANAL	P56093 candida alb
29	6	46.2	527	2 Q8VYH3	Q8VYH3 arabidopsis
30	6	46.2	528	1 AMY_BACCI	P08137 bacillus ci
31	6	46.2	552	2 Q9LVM8	Q9LVM8 arabidopsis

32	6	46.2	564	1 AMY4 SCHPO	Q9Y7S9 schizosacch
33	6	46.2	583	2 Q874K2	Q874K2 penicillium
34	6	46.2	604	1 RCO1 NEUCR	P78706 neurospora
35	6	46.2	604	2 Q7SBB8	Q7SBB8 neurospora
36	6	46.2	607	2 Q6BY06	Q6BY06 debaryomyce
37	6	46.2	614	1 TUI1 SCHPO	Q09715 schizosacch
38	6	46.2	619	2 Q6J0M8	Q6J0M8 exophiala d
39	6	46.2	619	2 Q9HGL0	Q9HGL0 emericella
40	6	46.2	624	1 AMY1 LIPKO	Q01117 lipomyces k
41	6	46.2	625	2 Q74922	Q74922 schizosacch
42	6	46.2	629	2 Q751E0	Q751E0 ashbya gos
43	6	46.2	631	2 Q92394	Q92394 cryptococcu
44	6	46.2	643	2 Q6FWR0	Q6FWR0 candida gla
45	6	46.2	647	2 Q8WZL8	Q8WZL8 yarrowia li

ALIGNMENTS

RESULT 1
ID AMYA ASPAW STANDARD; PRT; 498 AA.
AC Q02905;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DS glucanohydrolase A).
GN Name=AMVA;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JVK143F;
RX MEDLINE=90254827; PubMed=2340591;
RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
RT "Cloning, characterization, and expression of two alpha-amylase genes
from Aspergillus niger var. awamori.",
Curr. Genet. 17:203-212(1990).
RL
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -I- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -I- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X52755; CAA36966.1; -
CC FIR; A48305; A48305.
DR HSP; P10529; 7TAA.
DR InterPro: IPR006589; Alp amyl cat sub.
DR InterPro: IPR006047; Alpha_amyl_cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
KW Hydrolase; Multigene family; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 498 Alpha-amylase A.
FT ACT_SITE 227 227 Nucleophile (By similarity).
FT ACT_SITE 251 251 Proton donor (By similarity).
FT ACT_SITE 318 318 By similarity.
FT METAL 142 142 Calcium 1 (By similarity).

```

FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
FT METAL 196 196 Calcium 1 (By similarity).
FT METAL 227 227 Calcium 2 (By similarity).
FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
FT METAL 251 251 Calcium 2 (By similarity).
FT DISULFID 51 59 By similarity.
FT DISULFID 171 185 By similarity.
FT DISULFID 261 304 By similarity.
FT DISULFID 461 496 By similarity.
FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 498 AA; 54880 MW; 765851BC01A8A01 CRC64;

Query Match 100.0%; Score 13; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
| | | | | | | | | | |
DB 99 AYHGYWQDIYSL 111

RESULT 2
Q76CT3 PRELIMINARY; PRT; 498 AA.
AC Q76CT3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase.
GN Name=amyA;
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RA Ito K.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB109452; BAD01051.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amiyl_cat.
DR InterPro; IPR006589; Alp_amiyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 498 AA; 54679 MW; 8407BBFC7F4E3FC0 CRC64;

Query Match 100.0%; Score 13; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
| | | | | | | | | | |
DB 98 AYHGYWQDIYSL 110

RESULT 3
AMYA ASPOR STANDARD; PRT; 499 AA.
AC P10529; P11763; Q00250;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase A precursor (EC 3.2.1.1) (Taka-amylase A) (TAA) (1,4-
DE Alpha-D-glucan glucanohydrolase).
GN Name=AMY1;
GN and
GN Name=AMY2;

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GN and
GN Name=AMY3;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 63303;
RA MEDLINE=89237897; PubMed=2785629;
RA Wirsel S., Lachmund A., Wildhardt G., Ruttkowski E.;
RT "Three alpha-amylase genes of Aspergillus oryzae exhibit identical
RT intron-exon organization.";
RL Mol. Microbiol. 3:3-14(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6;
RA Genes M.J., Dove M.J., Seligy V.L.;
RT "Aspergillus oryzae has two nearly identical Taka-amylase genes, each
RT containing eight introns.";
RL Gene 79:107-117(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Tada S., Iimura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.;
RT "Cloning and nucleotide sequence of the genomic Taka-amylase A gene of
RT Aspergillus oryzae.";
RL Agric. Biol. Chem. 53:593-599(1989).
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
RA Tsukagoshi N., Furukawa M., Nagaba H., Kiritu N., Tsuboi A., Udaoka S.;
RT "Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A:
RT evidence for multiple related genes.";
RL Gene 84:319-327(1989).
RN [5]
RP SEQUENCE OF 22-499.
RA Toda H., Kondo K., Narita K.;
RT "The complete amino acid sequence of Taka-amylase A.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 58:208-212(1982).
RN [6]
RP SEQUENCE OF 206-225.
RA MEDLINE=74001521; PubMed=4733850;
RA Isemura S., Ikenaka T.;
RT "The amino acid sequences of glycopeptides obtained from Taka-amylase
RT A with trypsin and chymotrypsin.";
RL J. Biochem. 74:1-10(1973).
RN [7]
RP SEQUENCE OF 433-499.
RA Narita K.;
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RA MEDLINE=80227691; PubMed=6156152;
RA Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
RA Toda H., Narita K., Kakudo M.;
RT "Molecular structure of taka-amylase A. I. Backbone chain folding at
RT 3-A resolution.";
RL J. Biochem. 87:1555-1558(1980).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RA MEDLINE=84212370; PubMed=6609921;
RA Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
RT "Structure and possible catalytic residues of Taka-amylase A.";
RL J. Biochem. 95:697-702(1984).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
RA MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
RA Brzowski A.M., Davies G.J.;
RT "Structure of the Aspergillus oryzae alpha-amylase complexed with the
RT inhibitor acarbose at 2.0-A resolution.";
RL Biochemistry 36:10837-10845(1997).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.

```

CC -|- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations.
 CC -|- SUBUNIT: Monomer.
 CC -|- BIOTECHNOLOGY: Used in the brewing industry to increase the
 CC fermentability of beer worts (including those made from unmalted
 CC cereals), in the starch industry to make high maltose and high DE
 CC syrups (starch saccharification), in the alcohol industry to
 CC reduce fermentation time, in the cereal food industry for flour
 CC supplementation and improvement of chilled and frozen dough, and
 CC in the forestry industry for low-temperature modification of
 CC starch. Sold under the name Fungamyl by Novozymes.
 CC -|- MISCELLANEOUS: The sequence of AMY1 and AMY2 is shown.
 CC -|- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC -----
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 CC -----
 CC EMBL; X12725; CAA31218.1; --
 CC EMBL; X12726; CAA31219.1; --
 CC EMBL; X12727; CAA31220.1; --
 CC EMBL; D00434; BAA00336.1; --
 CC EMBL; M33218; AAA32708.1; --
 CC PIR; JK0201; JK0201.
 CC PIR; JT0466; JT0466.
 CC PIR; S04548; ALAS1.
 CC PDB; 2TAA; X-ray; A=22-499.
 CC PDB; 6TAA; X-ray; Q=22-499.
 CC PDB; 7TAA; X-ray; Q=22-499.
 CC GlycoSuiteDB; F10529; --
 CC InterPro; IPR006589; Alp_amy1_cat_sub.
 CC InterPro; IPR006047; Alpha_amy1_cat.
 CC InterPro; IPR006046; Glyco_hydro_13.
 CC Pfam; PF00128; Alpha-amy1ase; 1.
 CC PRINTS; PR00110; ALPHAAMYLAASE.
 CC SMART; SM00642; Amy; 1.
 CC 3D-structure; Calcium-binding; Carbohydrate metabolism;
 CC Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
 CC Multigene family; Signal.
 CC SIGNAL 1 21
 CC CHAIN 22 499 Alpha-amy1ase A.
 CC ACT_SITE 227 227 Nucleophile.
 CC ACT_SITE 251 251 Proton donor.
 CC ACT_SITE 318 318
 CC METAL 142 142 Calcium 1.
 CC METAL 183 183 Calcium 1 (via carbonyl oxygen).
 CC METAL 196 196 Calcium 1.
 CC METAL 227 227 Calcium 2.
 CC METAL 231 231 Calcium 1 (via carbonyl oxygen).
 CC METAL 251 251 Calcium 2.
 CC DISULFID 51 59
 CC DISULFID 171 185
 CC DISULFID 261 304
 CC DISULFID 461 496
 CC CARBOHYD 218 218 N-linked (GLCNAC...).
 CC VARIANT 56 56 Q -> R (in AMY3).
 CC VARIANT 172 172 F -> L (in AMY3).
 CC CONFLICT 93 94 TT -> DC (in Ref. 5).
 CC CONFLICT 106 106 Q -> T (in Ref. 5).
 CC CONFLICT 184 184 D -> Y (in Ref. 3).
 CC CONFLICT 195 195 P -> L (in Ref. 3).
 CC CONFLICT 255 255 G -> V (in Ref. 3).
 CC CONFLICT 291 291 D -> H (in Ref. 4).
 CC CONFLICT 345 345 I -> L (in Ref. 5).
 CC CONFLICT 370 370 L -> A (in Ref. 4).
 CC CONFLICT 406 409 WPY -> PYI (in Ref. 5).
 CC CONFLICT 448 448 G -> S (in Ref. 5).
 CC CONFLICT 497 497 S -> SD (in Ref. 5 and 7).

FT HELIX 24 27
 FT TURN 28 29
 FT STRAND 32 35
 FT HELIX 37 40
 FT STRAND 42 42
 FT TURN 43 44
 FT HELIX 53 55
 FT STRAND 61 61
 FT HELIX 63 68
 FT TURN 69 69
 FT HELIX 70 74
 FT TURN 75 77
 FT STRAND 80 83
 FT STRAND 87 89
 FT STRAND 94 94
 FT TURN 95 96
 FT STRAND 97 97
 FT TURN 100 101
 FT STRAND 105 111
 FT TURN 113 114
 FT HELIX 118 130
 FT TURN 131 132
 FT STRAND 134 139
 FT STRAND 143 143
 FT STRAND 146 148
 FT HELIX 150 152
 FT HELIX 155 157
 FT STRAND 159 159
 FT HELIX 164 166
 FT STRAND 167 167
 FT TURN 172 172
 FT TURN 176 177
 FT HELIX 184 188
 FT STRAND 186 188
 FT STRAND 192 194
 FT STRAND 195 197
 FT TURN 199 200
 FT HELIX 202 219
 FT TURN 220 220
 FT STRAND 223 226
 FT HELIX 229 231
 FT TURN 234 235
 FT HELIX 236 244
 FT TURN 245 245

Query Match 100.0%; Score 13; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 8.3e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
 |||||
 Db 99 AYHGYWQDIYSL 111

RESULT 4
 AMYB ASPAW STANDARD; PRT; 499 AA.
 ID AMYB ASPAW
 AC Q02906;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alpha-amy1ase B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase B).
 GN Name=AMYB;
 OS Aspergillus awamori.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=105351;
 RP [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=UVK143F;
 RX MEDLINE=90254827; PubMed=2340591;
 RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,

RA Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
 RT "Cloning, characterization, and expression of two alpha-amylase genes
 RL from *Aspergillus niger* var. *awamori*.";
 RL Curr. Genet. 17:203-212(1990).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations (By similarity).
 CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
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 CC -----
 DR EMBL; X52756; CAA36967.1; -.
 DR PIR; B48305; B48305.
 DR HSSP; P10529; 7TAA.
 DR InterPro; IPR006589; Alp amyl cat sub.
 DR InterPro; IPR006047; Alpha amyl cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 DR KMW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 KW Hydrolase; Multigene family; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 499 Alpha-amylase B.
 FT ACT_SITE 227 227 Nucleophile (By similarity).
 FT ACT_SITE 251 251 Proton donor (By similarity).
 FT ACT_SITE 318 318 By similarity.
 FT METAL 142 142 Calcium 1 (By similarity).
 FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 196 196 Calcium 1 (By similarity).
 FT METAL 227 227 Calcium 2 (By similarity).
 FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 251 251 Calcium 2 (By similarity).
 FT DISULFID 51 59 By similarity.
 FT DISULFID 171 185 By similarity.
 FT DISULFID 261 304 By similarity.
 FT DISULFID 461 496 By similarity.
 FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 499 AA; 54921 MW; 740B96B11BC01A8A CRC64;
 Query Match 100.0%; Score 13; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 8.3e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AVHGYWQDIYSL 13
 Db |||||
 Db 99 AVHGYWQDIYSL 111
 RESULT 5
 AMY_ASPSH STANDARD; PRT; 499 AA.
 ID ANY ASPSH
 AC P30292;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase).
 GN Name=AMY;
 OS Aspergillus shirousami.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eukaryotes; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5070;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=92323146; PubMed=1368777;
 RA Shibuya I., Tamura G., Ishikawa T., Hara S.;
 RT "Cloning of the alpha-amylase cDNA of *Aspergillus shirousami* and its
 RL expression in *Saccharomyces cerevisiae*.";
 RL Biosci. Biotechnol. Biochem. 56:174-179(1992).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations (By similarity).
 CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
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 CC -----
 DR EMBL; D10461; BAA01255.1; -.
 DR HSSP; P10529; 7TAA.
 DR InterPro; IPR006589; Alp amyl cat sub.
 DR InterPro; IPR006047; Alpha amyl cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 DR KMW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 KW Hydrolase; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 499 Alpha-amylase.
 FT ACT_SITE 227 227 Nucleophile (By similarity).
 FT ACT_SITE 251 251 Proton donor (By similarity).
 FT ACT_SITE 318 318 By similarity.
 FT METAL 142 142 Calcium 1 (By similarity).
 FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 196 196 Calcium 1 (By similarity).
 FT METAL 227 227 Calcium 2 (By similarity).
 FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 251 251 Calcium 2 (By similarity).
 FT DISULFID 51 59 By similarity.
 FT DISULFID 171 185 By similarity.
 FT DISULFID 261 304 By similarity.
 FT DISULFID 461 496 By similarity.
 FT CARBOHYD 218 218 N-linked (GlcNAc...) (By similarity).
 SQ SEQUENCE 499 AA; 54852 MW; 1FB7AE50DA01C03F CRC64;
 Query Match 100.0%; Score 13; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 8.3e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AVHGYWQDIYSL 13
 Db |||||
 Db 99 AVHGYWQDIYSL 111
 RESULT 6
 Q96TH4 PRELIMINARY; PRT; 499 AA.
 ID Q96TH4
 AC Q96TH4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Taka-amylase A (EC 3.2.1.1).
 DE Name=amyA;
 GN Aspergillus oryzae.
 OS Aspergillus oryzae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eukaryotes; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5062;
 RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN=RIE40;
RX MEDLINE=20289310; PubMed=10830498;
RA Gomi K., Akano T., Minetoki T., Ozeki K., Kumagai C., Okazaki N.,
RA Iimura Y.;
RT "Molecular cloning and characterization of a transcriptional activator
RT gene, amyR, involved in the amylolytic gene expression in Aspergillus
RT oryzae."
RL Biosci. Biotechnol. Biochem. 64:816-827(2000).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB021876; BAA95703.1; -.
DR PIR; JN0588; JN0588.
DR PIR; S04549; ALAS3.
DR HSP; P10529; 7TAA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; BEE42ADA71D20DA9 CRC64;

Query Match 100.0%; Score 13; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDDIYSL 13
Db |||||||||||

RESULT 7
Q76L99 PRELIMINARY; PRT; 499 AA.
AC Q76L99;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase precursor.
GN Name=amyl 1;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT-11;
RA Matsubara T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB083159; BA06002.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 499 AA; 54794 MW; 2B357AE38B36C1C2 CRC64;

Query Match 100.0%; Score 13; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDDIYSL 13
Db |||||||||||

RESULT 9
Q9UV07 PRELIMINARY; PRT; 490 AA.
AC Q9UV07;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha-amylase AmyA.
GN Name=amyA;
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
[1]
RP SEQUENCE FROM N.A.
RA Boase N.A., Murphy R.M., Kelly J.M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AF208225; AAF17103.1; -.
DR HSP; P10529; 7TAA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.

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Db 99 AYHGYYQDDIYSL 111

RESULT 8
Q7LV45 PRELIMINARY; PRT; 499 AA.
AC Q7LV45;
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
GN Name=amyl;
OS Aspergillus flavus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5059;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=86-10D;
RA Fakhoury A.M., Woloshuk C.P.;
RT "Amyl, the alpha-amylase gene of Aspergillus flavus: Involvement in
RT aflatoxin biosynthesis in maize kernels."
RL Phytopathology 89:908-914(1999).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AF139225; AAF14264.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;

Query Match 100.0%; Score 13; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDDIYSL 13
Db |||||||||||

RESULT 9
Q9UV07 PRELIMINARY; PRT; 490 AA.
AC Q9UV07;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha-amylase AmyA.
GN Name=amyA;
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
[1]
RP SEQUENCE FROM N.A.
RA Boase N.A., Murphy R.M., Kelly J.M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AF208225; AAF17103.1; -.
DR HSP; P10529; 7TAA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.

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DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 490 AA; 54249 MW; A891C4ACEABE5305 CRC64;

Query Match      84.6%; Score 11; DB 2; Length 490;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHGYWQDIY 11
   |||||
DB 91 AHGYWQDIY 101

RESULT 10
O15751 PRELIMINARY; PRT; 128 AA.
AC O15751;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AmyA (Fragment).
GN Name=amyA;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycotoxa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Loomis W.F., Iranfar N.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF020284; AAB70852.1; -.
DR HSSP; P10529; TAA.
DR DictyBase; DDB0214924; amyA.
DR GO; GO:0004556; F:alpha-amyase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_aml_cat.
DR Pfam; PF00128; Alpha-amyase; 1.
FT NON_TER 1
FT NON_TER 128
SQ SEQUENCE 128 AA; 14950 MW; 2ACE8FDC5E79637 CRC64;

Query Match      76.9%; Score 10; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YHGYWQDIY 11
   |||||
DB 3 YHGYWQDIY 12

RESULT 11
AMVA ASPNG STANDARD; PRT; 484 AA.
AC P56271;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acid alpha-amyase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=91002514; PubMed=2207069;
RA Boel E., Brady L., Brzozowski A.M., Derewenda Z., Dodson G.G.,
RA Jensen V.J., Petersen S.B., Swift H., Thim L., Woldike H.F.;
RT "Calcium binding in alpha-amyases: an X-ray diffraction study at 2.1-
RT A resolution of two enzymes from Aspergillus."
RL Biochemistry 29:6244-6249(1990).
CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -|- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations.
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CC -|- SUBUNIT: Monomer.
CC -|- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
DR PDB; 2AAA; X-ray; @=1-484.
DR InterPro; IPR006589; Alp_aml_cat_sub.
DR InterPro; IPR006047; Alpha_aml_cat.
DR Pfam; PF00128; Alpha-amyase; 1.
DR SMART; SM00642; Amy; 1.
KW 3D-structure; Calcium-binding; Carbohydrate metabolism; Glycoprotein;
KW Glycosidase; Hydrolase.
FT ACT_SITE 206 206 Nucleophile.
FT ACT_SITE 230 230 Proton donor.
FT ACT_SITE 297 297
FT METAL 121 121
FT METAL 162 162 Calcium 1.
FT METAL 175 175 Calcium 1.
FT METAL 206 206 Calcium 1.
FT METAL 210 210 Calcium 2.
FT METAL 230 230 Calcium 2.
FT DISULFID 30 38
FT DISULFID 150 164
FT DISULFID 240 283
FT DISULFID 440 475
FT CARBOHYD 24 24
FT CARBOHYD 157 157 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 197 197 N-linked (GlcNAc. . .) (Potential).
FT HELIX 3 6
FT TURN 7 8
FT STRAND 11 13
FT HELIX 16 19
FT TURN 22 23
FT HELIX 32 34
FT HELIX 42 47
FT TURN 48 48
FT TURN 49 53
FT TURN 54 56
FT STRAND 59 62
FT STRAND 66 68
FT STRAND 73 73
FT TURN 74 75
FT STRAND 76 76
FT TURN 79 80
FT STRAND 84 90
FT TURN 92 94
FT HELIX 97 108
FT TURN 109 111
FT STRAND 113 118
FT STRAND 122 122
FT STRAND 125 125
FT HELIX 129 131
FT HELIX 134 136
FT STRAND 138 138
FT HELIX 143 145
FT STRAND 146 146
FT STRAND 151 151
FT TURN 155 156
FT HELIX 158 163
FT STRAND 165 167
FT STRAND 172 173
FT STRAND 175 176
FT TURN 178 179
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FT TURN 199 199
FT STRAND 202 205
FT TURN 209 210
FT HELIX 213 215
FT HELIX 216 223
FT TURN 224 224
FT STRAND 226 229
FT HELIX 236 239
FT TURN 240 244
FT TURN 245 245
FT STRAND 248 250
FT HELIX 252 262
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FT TURN 265 266
FT HELIX 269 282
FT HELIX 286 288
FT STRAND 290 291
FT TURN 296 297
FT HELIX 301 303
FT TURN 304 304
FT HELIX 308 320
FT STRAND 324 328
FT TURN 329 334
FT TURN 339 343
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FT TURN 354 355
FT HELIX 357 375
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FT STRAND 385 390
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FT STRAND 393 398
FT TURN 401 403
FT STRAND 405 410
FT TURN 414 415
FT STRAND 419 423
FT TURN 430 431
FT STRAND 433 436
FT TURN 437 440
FT STRAND 441 444
FT TURN 447 448
FT STRAND 451 455
FT TURN 457 458
FT STRAND 461 465
FT HELIX 466 469
FT TURN 470 471
FT TURN 474 475
SQ SEQUENCE 484 AA; 52935 MW; 04D596E34680656D CRC64;

Query Match 61.5%; Score 8; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.38; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQQ 8
|||||||
Db 78 AYHGYWQQ 85

RESULT 12
Q76L96 PRELIMINARY; PRT; 634 AA.
AC Q76L96;
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylose precursor.
GN Name=amyl III;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT-11;
RA Matsubara T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083162; BAD06005.1; -.
DR EMBL; AB083160; BAD06003.1; -.
DR HSSP; P04064; IACZ.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_aml cat.
DR InterPro; IPR006589; Alp_aml cat sub.
DR InterPro; IPR002044; Glyco_hydro_CBD.
DR Pfam; PF00128; Alpha-amylose; 1.
DR ProDom; PD001568; Glyco_Hydro_CBD; 1.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 640 AA; 69507 MW; 676BF9D0236720DD CRC64;

Query Match 61.5%; Score 8; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.38; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQQ 8
|||||||
Db 78 AYHGYWQQ 85

DR Pfam; PF00686; CBM_20; 1.
DR ProDom; PD001568; Glyco_Hydro_CBD; 1.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL 1 21 Potential.
SQ SEQUENCE 634 AA; 69242 MW; 16C0BE6AF6B0B9B CRC64;
Query Match 61.5%; Score 8; DB 2; Length 634;
Best Local Similarity 100.0%; Pred. No. 0.46; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQQ 8
|||||||
Db 99 AYHGYWQQ 106

RESULT 13
O13296 PRELIMINARY; PRT; 640 AA.
AC O13296;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acid-stable alpha-amylose.
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaneko A., Sudo S., Sakamoto Y., Tamura G., Ishikawa T., Ohba T.;
RT "Molecular-cloning and determination of the nucleotide-sequence of a
RT gene encoding an acid-stable alpha-amylose from Aspergillus-
RT kawachi.",
RL J. Ferment. Bioeng. 81:292-298(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Kaneko A.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB008370; BAA22993.1; -.
DR HSSP; P56271; 2AAA.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_aml cat.
DR InterPro; IPR006589; Alp_aml cat sub.
DR InterPro; IPR002044; Glyco_hydro_CBD.
DR Pfam; PF00128; Alpha-amylose; 1.
DR ProDom; PD001568; Glyco_Hydro_CBD; 1.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 640 AA; 69507 MW; 676BF9D0236720DD CRC64;

Query Match 61.5%; Score 8; DB 2; Length 640;
Best Local Similarity 100.0%; Pred. No. 0.46; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQQ 8
|||||||
Db 99 AYHGYWQQ 106

RESULT 14
Q6Y198 PRELIMINARY; PRT; 322 AA.
AC Q6Y198;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE TUP1-like protein (Fragment).
OS Pichia angusta (Yeast) (Hansenula polymorpha).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.

Search completed: November 7, 2005, 19:32:39
Job time : 7.90154 secs

OX NCBI_TaxID=4905;
RN [1]
RP SEQUENCE FROM N.A.
RA Oliveira M.A., Salmazo A.P.T., Faria V.G., Pereira G.A.G.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 7 WD repeats.
DR EMBL; AV145087; AAN60571.1; -.
DR InterPro; IPR001690; WD40.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINRPT.
DR ProDom; PD000018; WD40; 6.
DR SMART; SM00320; WD40; 6.
DR PROSITE; PS00678; WD_REPEATS_1; 3.
DR PROSITE; PS00082; WD_REPEATS_2; 6.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT NON_TER 1
FT NON_TER 322 322
SQ SEQUENCE 322 AA; 35083 MW; 017CADD0E0E9B03 CRC64;

Query Match 46.2%; Score 6; DB 2; Length 322;
Best Local Similarity 100.0%; Pred.No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QDIYSL 13
Db 99 QDIYSL 104

RESULT 15
Q9M6R9 PRELIMINARY; PRT; 413 AA.
AC Q9M6R9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
OS Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fruit;
RX MEDLINE=20156234; PubMed=10691968;
RA Wegrzyn T., Reilly K., Cipriani G., Murphy P., Newcomb R., Gardner R.,
RA MacRae E.;
RT "A novel alpha-amylase gene is transiently upregulated during low
RT temperature exposure in apple fruit.";
RL Eur. J. Biochem. 257:1313-1322(2000).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AF153828; AAF63239.1; -.
DR HSSP; P04063; 1BG9.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 413 AA; 46883 MW; C77763D797B6D0EA CRC64;

Query Match 46.2%; Score 6; DB 2; Length 413;
Best Local Similarity 100.0%; Pred.No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QDIYSL 13
Db 77 QDIYSL 82

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:24:00 ; Search time 3.75676 Seconds
(without alignments)
954.162 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167
Perfect score: 40
Sequence: 1 SSQDYFH 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	40	100.0	498	1 AMYA ASPAW	Q02905 aspergillus
2	40	100.0	498	2 Q76CT3	Q76ct3 aspergillus
3	40	100.0	499	1 AMYA ASPOR	P10529 aspergillus
4	40	100.0	499	1 AMYA ASPAW	Q02906 aspergillus
5	40	100.0	499	1 AMY ASPSH	P30292 aspergillus
6	40	100.0	499	2 Q96TH4	Q96th4 aspergillus
7	40	100.0	499	2 Q76L99	Q76l99 aspergillus
8	40	100.0	499	2 Q7LV45	Q7lv45 aspergillus
9	40	100.0	624	1 AMY1 LIPKO	Q01117 lipomyces k
10	40	100.0	647	2 Q6YF33	Q6yf33 lipomyces s
11	37	92.5	224	2 Q70BE3	Q70be3 pseudomonas
12	36	90.0	596	2 Q7BL16	Q7bl16 plasmodium
13	36	90.0	627	2 Q6ENF7	Q6enf7 candida gla
14	35	87.5	760	2 Q7R038	Q7r038 giardia lam
15	35	87.5	760	2 Q9XZJ0	Q9xzt0 giardia lam
16	34	85.0	130	2 Q23373	Q23373 arabidopsis
17	34	85.0	7048	2 Q6D739	Q6d739 erwinia car
18	33	82.5	125	2 Q751X1	Q751x1 ashbya gos
19	33	82.5	193	2 Q8LMS1	Q8lms1 oryza sativ
20	33	82.5	248	2 Q7YSZ6	Q7ysz6 rhodnus pr
21	33	82.5	257	2 Q6P396	Q6p396 mus musculu
22	33	82.5	370	2 Q8BYC0	Q8byc0 mus musculu
23	33	82.5	420	2 Q39309	Q39309 equid herpe
24	33	82.5	420	2 Q55525	Q55525 equid herpe
25	33	82.5	585	1 CT9 MOUSE	Q9d718 mus musculu
26	33	82.5	601	2 O17552	O17552 caenorhabdi
27	33	82.5	762	2 Q7NAH6	Q7nah6 mycoplasma
28	33	82.5	1131	1 DNEB1 HHV7J	P52339 human herpe
29	33	82.5	1131	2 Q56282	Q56282 human herpe
30	33	82.5	1304	2 Q6FR07	Q6fr07 candida gla
31	33	82.5	1731	2 Q9P230	Q9p230 homo sapien

32	33	82.5	3124	2	Q96L91	Q96l91 homo sapien
33	33	82.5	4351	1	FAT2_RAT	O88277 rattus norv
34	32	80.0	49	2	Q6XYZ7	Q6xyz7 spiroplasma
35	32	80.0	95	2	Q7RM89	Q7rm89 plasmodium
36	32	80.0	144	1	AGH ARMVU	Q9u8r2 armadillidi
37	32	80.0	163	2	Q9CUQ8	Q9cuq8 mus musculu
38	32	80.0	180	2	Q97SK2	Q97sk2 streptococc
39	32	80.0	181	2	Q7USU1	Q7usu1 rhodopirell
40	32	80.0	183	2	Q8DZ39	Q8dz39 streptococc
41	32	80.0	183	2	Q8E4P7	Q8e4p7 streptococc
42	32	80.0	215	2	P97975	P97975 unidentified
43	32	80.0	218	2	Q9CUH8	Q9cuh8 mus musculu
44	32	80.0	255	2	Q8EU15	Q8eu15 oceanobacil
45	32	80.0	261	2	Q73L56	Q73l56 treponema d

ALIGNMENTS

RESULT 1

AMYA ASPAW STANDARD; PRT; 498 AA.
AC Q02905;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase A).
GN Name=AMYA;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=UVK143F;
RC MEDLINE=90254827; PubMed=2340591;
RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
RT "Cloning, characterization, and expression of two alpha-amylase genes
RT from Aspergillus niger var. awamori.",
RL Curr. Genet. 17:203-212(1990).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X52755; CAA36966.1; -;
CC PIR; A48305; A48305.
CC HSP; P10529; 7TAA.
CC InterPro; IPR006589; Alp_ amyl_cat_sub.
CC InterPro; IPR006047; Alpha_ amyl_cat.
CC InterPro; IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; Alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAAMYLASE.
CC SMART; SM00642; Amyv; 1.
CC Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
CC Hydroxylase; Multigene family; Signal.
CC SIGNAL 1 21
CC CHAIN 22 498
CC ACT_SITE 227 227 Nucleophile (By similarity).
CC ACT_SITE 251 251 Proton donor (By similarity).
CC ACT_SITE 318 318 By similarity.
CC METAL 142 142 Calcium 1 (By similarity).

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FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
FT METAL 196 196 similarity).
FT METAL 227 227 Calcium 1 (By similarity).
FT METAL 231 231 Calcium 2 (By similarity).
FT METAL 251 251 Calcium 1 (via carbonyl oxygen) (By
FT METAL 251 251 similarity).
FT DISULFID 51 59 Calcium 2 (By similarity).
FT DISULFID 171 185 By similarity.
FT DISULFID 261 304 By similarity.
FT DISULFID 461 496 By similarity.
FT CARBOHYD 218 218 By similarity.
SQ SEQUENCE 498 AA; 54880 MW; 765851BC01A9A01 CRC64;

Query Match 100.0%; Score 40; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 2
O76CT3 PRELIMINARY; PRT; 498 AA.
AC O76CT3;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Alpha-amyase.
GN Name=amyA;
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RA Ito K.;
RP Submitted (MAY-2003) to the EMBL/GenBank/DBSJ databases.
RL -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC EMBL; AB109452; BAD01051.1; -.
DR GO; GO:0004556; F:alpha-amyase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_aml cat.
DR InterPro; IPR006589; Alp_aml_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 498 AA; 54679 MW; 8407BBFC7F4E3FC0 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSQDYFH 7
Db 161 SSQDYFH 167

RESULT 3
AMYA ASPOR STANDARD; PRT; 499 AA.
AC P10529; P11763; Q00250;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amyase A precursor (EC 3.2.1.1) (Taka-amyase A) (TAA) (1,4-
DE alpha-D-glucan glucanohydrolase).
GN Name=AMY1;
GN and
GN Name=AMY2;

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GN and
GN Name=AMY3;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 63303;
RC MEDLINE=89237897; PubMed=2785629;
RA Wiersel S., Lachmund A., Wildhardt G., Rutkowski E.;
RA "Three alpha-amyase genes of Aspergillus oryzae exhibit identical
RT intron-exon organization.";
RL Mol. Microbiol. 3:3-14(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6;
RA Genes M.J., Dove M.J., Seligy V.L.;
RA "Aspergillus oryzae has two nearly identical Taka-amyase genes, each
RT containing eight introns.";
RL Gene 79:107-117(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Tada S., Iimura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.;
RT "Cloning and nucleotide sequence of the genomic Taka-amyase A gene of
RL Aspergillus oryzae.";
RL Agric. Biol. Chem. 53:593-599(1989).
RN [4]
RP SEQUENCE FROM N.A.
RC MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
RA Tsukagoshi N., Furukawa M., Nagaba H., Kirita N., Tsuboi A., Udaoka S.;
RT "Isolation of a cDNA encoding Aspergillus oryzae Taka-amyase A:
RL evidence for multiple related genes.";
RN [5]
RP SEQUENCE OF 22-499.
RA Toda H., Kondo K., Narita K.;
RT "The complete amino acid sequence of Taka-amyase A.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 58:208-212(1982).
RN [6]
RP SEQUENCE OF 206-225.
RX MEDLINE=74001521; PubMed=4733850;
RA Isemura S., Ikenaka T.;
RT "The amino acid sequences of glycopeptides obtained from Taka-amyase
RL A with trypsin and chymotrypsin.";
RL J. Biochem. 74:1-10(1973).
RN [7]
RP SEQUENCE OF 433-499.
RA Narita K.;
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=80227691; PubMed=6156152;
RA Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
RA Toda H., Narita K., Kakudo M.;
RT "Molecular structure of taka-amyase A. I. Backbone chain folding at
RT 3-A resolution.";
RL J. Biochem. 87:1555-1558(1980).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=84212370; PubMed=6609921;
RA Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
RT "Structure and possible catalytic residues of Taka-amyase A.";
RL J. Biochem. 95:697-702(1984).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
RX MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
RA Brzozowski A.M., Davies G.J.;
RT "Structure of the Aspergillus oryzae alpha-amyase complexed with the
RT inhibitor acarbose at 2.0-A resolution.";
RL Biochemistry 36:10837-10845(1997).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.

```

CC -|- COPACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations.
 CC -|- SUBUNIT: Monomer.
 CC -|- BIOTECHNOLOGY: Used in the brewing industry to increase the
 CC fermentability of beer worts (including those made from unmalted
 CC cereals), in the starch industry to make high maltose and high DE
 CC syrups (starch saccharification), in the alcohol industry to
 CC reduce fermentation time, in the cereal food industry for flour
 CC supplementation and improvement of chilled and frozen dough, and
 CC in the forestry industry for low-temperature modification of
 CC starch. Sold under the name Fungamyl by Novozymes.
 CC -|- MISCELLANEOUS: The sequence of AMY1 and AMY2 is shown.
 CC -|- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X12725; CAA31218.1; -;
 CC EMBL; X12726; CAA31219.1; -;
 CC EMBL; X12727; CAA31220.1; -;
 CC EMBL; D00434; BAA00336.1; -;
 CC EMBL; M33218; AAA32708.1; -;
 CC PIR; JK0201; JK0201.
 CC PIR; JT0466; JT0466.
 CC PIR; S04548; ALAS1.
 CC PDB; 2TAA; X-ray; A=22-499.
 CC PDB; 6TAA; X-ray; @=22-499.
 CC PDB; 7TAA; X-ray; @=22-499.
 CC GlycoSuiteDB; P10529; -;
 CC InterPro; IPR006589; Alp_amy1_cat_sub.
 CC InterPro; IPR006047; Alpha_amy1_cat.
 CC InterPro; IPR006046; Glyco_hydro_13.
 CC Pfam; PF00128; Alpha-amy1ase; 1.
 CC PRINTS; PR00110; ALPHAAMYLAASE.
 CC SMART; SM00642; Aamy; 1.
 CC 3D-structure; Calcium-binding; Carbohydrate metabolism;
 KW Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
 KW Multigene family; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 499 Alpha-amy1ase A.
 FT ACT_SITE 227 227 Nucleophile.
 FT ACT_SITE 251 251 Proton donor.
 FT ACT_SITE 318 318
 FT METAL 142 142 Calcium 1.
 FT METAL 183 183 Calcium 1 (via carbonyl oxygen).
 FT METAL 196 196 Calcium 1.
 FT METAL 227 227 Calcium 2.
 FT METAL 231 231 Calcium 1 (via carbonyl oxygen).
 FT METAL 251 251 Calcium 2.
 FT DISULFID 51 59
 FT DISULFID 171 185
 FT DISULFID 261 304
 FT DISULFID 461 496
 FT CARBOHYD 218 218 N-linked (GlcNAc...).
 FT VARIANT 56 56 /FTID-CAR_000125.
 FT VARIANT 172 172 Q -> R (in AMY3).
 FT CONFLICT 93 94 F -> L (in AMY3).
 FT CONFLICT 106 106 TT -> DC (in Ref. 5).
 FT CONFLICT 184 184 Q -> T (in Ref. 5).
 FT CONFLICT 185 184 D -> Y (in Ref. 3).
 FT CONFLICT 195 195 P -> L (in Ref. 3).
 FT CONFLICT 255 255 D -> V (in Ref. 3).
 FT CONFLICT 291 291 D -> H (in Ref. 4).
 FT CONFLICT 345 345 I -> L (in Ref. 5).
 FT CONFLICT 370 370 L -> A (in Ref. 4).
 FT CONFLICT 406 409 WPIY -> PYI (in Ref. 5).
 FT CONFLICT 448 448 G -> S (in Ref. 5).
 FT CONFLICT 497 497 S -> SD (in Ref. 5 and 7).

FT HELIX 24 27
 FT TURN 28 29
 FT STRAND 32 35
 FT HELIX 37 40
 FT STRAND 42 42
 FT TURN 43 44
 FT HELIX 53 55
 FT STRAND 61 61
 FT HELIX 63 68
 FT TURN 69 69
 FT HELIX 70 74
 FT TURN 75 77
 FT STRAND 80 83
 FT STRAND 87 89
 FT STRAND 94 94
 FT TURN 95 96
 FT STRAND 97 97
 FT TURN 100 101
 FT STRAND 105 111
 FT TURN 113 114
 FT HELIX 118 130
 FT TURN 131 132
 FT STRAND 134 139
 FT STRAND 143 143
 FT STRAND 146 148
 FT HELIX 150 152
 FT HELIX 155 157
 FT STRAND 159 159
 FT STRAND 164 166
 FT HELIX 167 167
 FT STRAND 172 172
 FT TURN 176 177
 FT HELIX 179 184
 FT STRAND 186 188
 FT STRAND 192 194
 FT STRAND 196 197
 FT TURN 199 200
 FT TURN 202 219
 FT TURN 220 220
 FT STRAND 223 226
 FT HELIX 229 231
 FT TURN 234 235
 FT HELIX 236 244
 FT TURN 245 245

Query Match 100.0%; Score 40; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||
 Db 162 SSQDYFH 168

RESULT 4
 AMYB ASPAW
 ID AMYB ASPAW STANDARD; PRT; 499 AA.
 AC Q02906;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alpha-amy1ase B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase B).
 GN Name=AMYB;
 OS Aspergillus awamori.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=105351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UVK143F;
 RX MEDLINE=90254827; PubMed=2340591;
 RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,


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RP SEQUENCE FROM N.A.
RC STRAIN=RIB40;
RX MEDLINE=20289310; PubMed=10830498;
RA Gomi K., Akeno T., Minetoki T., Ozeki K., Kumagai C., Okazaki N.,
RA Iimura Y.;
RT "Molecular cloning and characterization of a transcriptional activator
RT gene, amyR, involved in the amylolytic gene expression in Aspergillus
RT oryzae.";
CC BLAST: Biotechnol. Biochem. 64:816-827(2000).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB021876; BAA95703.1; -.
DR PIR; JN0588; JN0588.
DR PIR; S04549; ALAS3.
DR HSP; P10529; TAA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Aamy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 162 SSQDYFH 168

RESULT 7
Q76L99 PRELIMINARY; PRT; 499 AA.
AC Q76L99;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase precursor.
DE Name=amyl I;
GN Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eukaryotes; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT-11;
RA Matsubara T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB083159; BAD06002.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Aamy; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 499 AA; 54794 MW; 2B357AE38B36C1C2 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 162 SSQDYFH 168
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Db 162 SSQDYFH 168

RESULT 8
Q7LV45 PRELIMINARY; PRT; 499 AA.
AC Q7LV45;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
DE Name=amyl;
OS Aspergillus flavus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eukaryotes; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5059;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=86-10D;
RA Fakhoury A.M., Woloshuk C.P.;
RT "Amyl, the alpha-amylase gene of Aspergillus flavus: Involvement in
RT aflatoxin biosynthesis in maize kernels.";
RL Phytotechnology 89:908-914(1999).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AF139925; AAF14264.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Aamy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 162 SSQDYFH 168

RESULT 9
AMYL_LIPKO STANDARD; PRT; 624 AA.
AC Q01117;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase 1).
DE Name=LKAl;
OS Lipomyces kononenkoae.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Lipomycetaceae; Lipomyces.
OX NCBI_TaxID=34357;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IGC4052B;
RX MEDLINE=96105202; PubMed=8529895; DOI=10.1016/0378-1119(95)00633-0;
RA Steyn A.J.C., Marmur J., Pretorius I.S.;
RT "Cloning, sequence analysis and expression in yeasts of a cDNA
RT containing a Lipomyces kononenkoae alpha-amylase-encoding gene.";
RL Gene 166:65-71(1995).
RN [2]
RP SEQUENCE OF 29-44.
RC STRAIN=IGC4052B;
RX MEDLINE=96132108; PubMed=8593683;
RA Steyn A.J.C., Pretorius I.S.;
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RT "Characterization of a novel alpha-amylase from *Lipomyces kononenkoae*
 RL and expression of its gene (LKAL) in *Saccharomyces cerevisiae*.";
 CC Curr. Genet. 28:526-533(1995).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC -!- SIMILARITY: Contains 1 carbohydrate binding type-21 (CBM21)
 CC domain.
 CC -----
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 CC -----
 CC EMBL; U30376; AAC49622.1; ALT_INIT.
 CC PIR; JC4510; JC4510.
 CC DR HSP; P10529; 7TAA.
 CC DR InterPro; IPR006589; Alp_amyl_cat_sub.
 CC DR InterPro; IPR006047; Alpha_amyl_cat.
 CC DR InterPro; IPR005036; CBM 21.
 CC DR Pfam; PF00128; Alpha-amylase; 1.
 CC DR Pfam; PF03370; CBM 21; 1.
 CC DR SMART; SM00642; Aamy; 1.
 CC DR Calcium-binding; Carbohydrate metabolism; Direct protein sequencing;
 KW Glycoprotein; Glycosidase; Hydrolase; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 624 Alpha-amylase 1.
 FT DOMAIN 40 133 Carbohydrate binding type-21.
 FT ACT_SITE 353 Nucleophile (By similarity).
 FT ACT_SITE 377 Proton donor (By similarity).
 FT ACT_SITE 444 By similarity.
 FT METAL 268 Calcium 1 (By similarity).
 FT METAL 309 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 322 Calcium 1 (By similarity).
 FT METAL 353 Calcium 2 (By similarity).
 FT METAL 357 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 377 Calcium 2 (By similarity).
 FT DISULFID 177 185 By similarity.
 FT DISULFID 297 311 By similarity.
 FT DISULFID 387 430 By similarity.
 FT DISULFID 587 622 By similarity.
 FT CARBOHYD 304 304 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 344 344 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 624 AA; 68876 MW; 87EB16534F5A9A9F CRC64;

Query Match 100.0%; Score 40; DB 1; Length 624;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 Db 288 SSQDYFH 294
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RESULT 10
 Q6YF33 PRELIMINARY; PRT; 647 AA.
 AC Q6YF33;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Alpha-amylase.
 OS *Lipomyces starkeyi*.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Lipomycetaceae; *Lipomyces*.

OX NCBI_TaxID=29829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KSM 22M;
 RX PubMed=15043869; DOI=10.1016/j.femsle.2004.01.036;
 RA Kang H.K., Lee J.H., Kim D., Day D.F., Robyt J.F., Park K.-H.,
 RA Moon T.-W.;
 RT "Cloning and expression of *Lipomyces starkeyi* alpha-amylase in
 RT *Escherichia coli* and determination of some of its properties.";
 RL FEMS Microbiol. Lett. 233:53-64(2004).
 DR EMBL; AY155463; AAN75021.1; --
 DR HSP; P26827; 1A47.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR InterPro; IPR005036; CBM 21.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR Pfam; PF03370; CBM 21; 1.
 DR SMART; SM00642; Aamy; 1.
 SQ SEQUENCE 647 AA; 70957 MW; D946071DB7560144 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 647;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 Db 311 SSQDYFH 317
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RESULT 11
 Q70BE3 PRELIMINARY; PRT; 224 AA.
 ID Q70BE3
 AC Q70BE3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative helicase.
 OS *Pseudomonas syringae* (pv. tomato).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; *Pseudomonas*.
 OX NCBI_TaxID=323;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Panelli V., Finetti-Sialer M., Gallitelli D.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AJ604569; CAES4310.1; --
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00271; Helicase_C; 1.
 KW Helicase.
 SQ SEQUENCE 224 AA; 25431 MW; 8701280423194015 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 224;
 Best Local Similarity 85.7%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 Db 130 STQDYFH 136
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RESULT 12
 Q7RL16 PRELIMINARY; PRT; 596 AA.
 ID Q7RL16
 AC Q7RL16;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE *Drosophila melanogaster* CG11926 gene product, putative


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DE (Fragment).
DN Name=PY02732;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=1236865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguolli S.V., Suh B.B., Kooij T.W., Perteu M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosak D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519 (2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABL01000756; EAA22214.1; -.
DR InterPro: IPR004353; Yeast73DUF.
DR Pfam: PF03164; DUF254; 1.
DR PRINTS: PR01546; YEAST73DUF.
FT NON TER 1
SQ SEQUENCE 596 AA; 69216 MW; 8170C2D33F53117D CRC64;

Query Match 90.0%; Score 36; DB 2; Length 596;
Best Local Similarity 85.7%; Pred. No. 87;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 446 SSQDFFH 452

RESULT 13
ID Q6FNF7 PRELIMINARY; PRT; 627 AA.
AC Q6FNF7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Candida glabrata strain CBS138 chromosome K complete sequence.
GN ORFNames=CAGL0K002979;
OS Candida glabrata CBS138.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=284593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Algic M., Anchoard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrast A., Koszul R., Lemaire M., Lesur J., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";

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RL Nature 430:35-44 (2004).
DR EMBL: CR380957; CAG61198.1; -.
DR InterPro: IPR002013; SyJa_N.
DR Pfam: PF02383; SyJa_N; 1.
DR PROSITE: PS0275; SAC; 1.
SQ SEQUENCE 627 AA; 71471 MW; DEA0B02466F4F480 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 627;
Best Local Similarity 85.7%; Pred. No. 92;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 365 SSQDYFH 371

RESULT 14
QYR038 PRELIMINARY; PRT; 760 AA.
ID QYR038;
AC QYR038;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP 456 15756 18038.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OC NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AACB01000038; EAA40649.1; -.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00223; ANK; 3.
DR PRINTS: PR01415; ANKYRIN.
SQ SEQUENCE 760 AA; 85474 MW; A01440ACE754099C CRC64;

Query Match 87.5%; Score 35; DB 2; Length 760;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 5 SSQDWFH 11

RESULT 15
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ID QYXZJ0;
AC QYXZJ0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ankyrin-like protein.
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Portland;
RA Sekyere E.O., Edwards M.R., Stewart T.S., Schofield P.J., Knodler L.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF144322; AAD28486.1; -.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ANK; 3.
DR PRINTS: PR01415; ANKYRIN.
DR SMART: SM00248; ANK; 3.

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KW ANK repeat.
SQ SEQUENCE 760 AA; 85542 MW; 12B54841019CD475 CRC64;
Query Match 87.5%; Score 35; DB 2; Length 760;
Best Local Similarity 85.7%; Pred. NO. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
Db 5 SSQDWFH 11

Search completed: November 7, 2005, 18:52:32
Job time : 5.75676 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 17:47:24 ; Search time 1.05405 Seconds
(without alignments)
495.746 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167

Perfect score: 40

Sequence: 1 SSQDYFH 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/1aa/5B-COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A-COMB.pep:*
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5: /cgn2_6/prodata/1/1aa/PTUS-COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	478	1	US-08-720-899-7
2	40	100.0	478	1	US-08-459-610-7
3	40	100.0	478	2	US-08-343-804-7
4	40	100.0	478	2	US-08-339-715A-2
5	40	100.0	478	2	US-08-600-908A-10
6	40	100.0	478	3	US-08-683-838A-10
7	40	100.0	478	3	US-09-182-859-7
8	40	100.0	478	4	US-09-672-459-7
9	40	100.0	478	4	US-09-636-252A-10
10	40	100.0	478	4	US-10-186-042-7
11	33	82.5	180	4	US-09-248-796A-22820
12	32	80.0	84	4	US-09-583-110-4016
13	32	80.0	95	4	US-09-107-433-4442
14	32	80.0	369	1	US-08-700-359-21
15	32	80.0	583	2	US-08-616-392C-4
16	32	80.0	788	4	US-09-107-532A-6538
17	32	80.0	792	4	US-09-134-000C-5895
18	32	80.0	820	2	US-08-380-182-23
19	32	80.0	1118	4	US-09-949-016-6596
20	32	80.0	1120	4	US-09-949-016-10404
21	31	77.5	153	4	US-09-328-352-4170
22	31	77.5	279	4	US-09-270-767-34772
23	31	77.5	279	4	US-09-270-767-49989
24	31	77.5	461	4	US-09-198-452A-924
25	31	77.5	472	4	US-09-438-185A-858
26	31	77.5	474	4	US-09-081-385-148
27	31	77.5	2697	4	US-10-144-198-12

28	30	75.0	25	1	US-08-485-455D-41	Sequence 41, Appl
29	30	75.0	25	2	US-08-482-130C-41	Sequence 41, Appl
30	30	75.0	25	2	US-08-484-211C-41	Sequence 41, Appl
31	30	75.0	25	3	US-08-906-769-41	Sequence 41, Appl
32	30	75.0	25	3	US-08-906-616-41	Sequence 41, Appl
33	30	75.0	25	3	US-08-817-795-41	Sequence 41, Appl
34	30	75.0	25	3	US-08-485-443B-41	Sequence 41, Appl
35	30	75.0	25	3	US-08-639-075A-41	Sequence 41, Appl
36	30	75.0	25	3	US-09-012-431-41	Sequence 41, Appl
37	30	75.0	25	3	US-09-012-692-41	Sequence 41, Appl
38	30	75.0	25	3	PCT-US95-14442A-41	Sequence 41, Appl
39	30	75.0	25	5	US-08-485-455D-75	Sequence 75, Appl
40	30	75.0	64	1	US-08-482-130C-75	Sequence 75, Appl
41	30	75.0	64	2	US-08-482-130C-75	Sequence 75, Appl
42	30	75.0	64	2	US-08-906-769-75	Sequence 75, Appl
43	30	75.0	64	3	US-08-906-616-75	Sequence 75, Appl
44	30	75.0	64	3	US-08-817-795-75	Sequence 75, Appl
45	30	75.0	64	3	US-08-817-795-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1
US-08-720-899-7
; Sequence 7, Application US/08720899
; Patent No. 5753460
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57534600 No. 5753460disk of No. 5753460th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,899
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-720-899-7

Query Match 100.0%; Score 40; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 2
US-08-459-610-7
; Sequence 7, Application US/08459610
; Patent No. 5801043
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 5801043o No. 5801043disk of No. 5801043th America, Inc.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; APPLICATION NUMBER: US/08/459,610
; FILING DATE: 02-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-459-610-7

Query Match 100.0%; Score 40; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 3
US-08-343-804-7
; Sequence 7, Application US/08343804
; Patent No. 5830837
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 5830837o No. 5830837disk of No. 5830837th America, Inc.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; APPLICATION NUMBER: US/08/339,715A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306096/1993

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 4
US-08-339-715A-2
; Sequence 2, Application US/08339715A
; Patent No. 5965442
; GENERAL INFORMATION:
; APPLICANT: Kaneko, Hiroki
; APPLICANT: Takada, Toshikazu
; APPLICANT: Shimada, Jiro
; APPLICANT: Kuriaki, Takashi
; APPLICANT: Yanase, Michio
; APPLICANT: Takata, Hiroki
; APPLICANT: Okada, Shigetaka
; TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
; STREET: Metropolitan Square Building, Suite 800, 1450
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,715A
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306096/1993

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 5
US-08-339-715A-2
; Sequence 2, Application US/08339715A
; Patent No. 5965442
; GENERAL INFORMATION:
; APPLICANT: Kaneko, Hiroki
; APPLICANT: Takada, Toshikazu
; APPLICANT: Shimada, Jiro
; APPLICANT: Kuriaki, Takashi
; APPLICANT: Yanase, Michio
; APPLICANT: Takata, Hiroki
; APPLICANT: Okada, Shigetaka
; TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
; STREET: Metropolitan Square Building, Suite 800, 1450
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,715A
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306096/1993
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; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Melse, Allen S.
; REGISTRATION NUMBER: 27,215
; REFERENCE/DOCKET NUMBER: 18335.009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-824-8000
; TELEFAX: 202-824-8199
; TELEX: 248516
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-339-715A-2

Query Match 100.0%; Score 40; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 141 SSQDYFH 147

RESULT 5
US-08-600-908A-10
; Sequence 10, Application US/08600908A
; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: '-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5989169o No. 5989169th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-600-908A-10

Query Match 100.0%; Score 40; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 141 SSQDYFH 147

RESULT 7
US-09-182-859-7
; Sequence 7, Application US/09182859
; Patent No. 6143708
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisg rd-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/182,859
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: 0515/96
; EARLIER FILING DATE: 1996-04-30
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; EARLIER APPLICATION NUMBER: 0712/96
; EARLIER FILING DATE: 1996-06-28
; EARLIER APPLICATION NUMBER: 0775/96
; EARLIER FILING DATE: 1996-07-11
; EARLIER APPLICATION NUMBER: 1263/96
; EARLIER FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-182-859-7
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Query Match 100.0%; Score 40; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147
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RESULT 8
US-09-672-459-7
; Sequence 7, Application US/09672459
; Patent No. 6436888
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-672-459-7
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Query Match 100.0%; Score 40; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147
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RESULT 9
US-09-636-252A-10
; Sequence 10, Application US/09636252A
; Patent No. 6440716
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/09/636,252A
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; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-09-636-252A-10
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Query Match 100.0%; Score 40; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147
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RESULT 10
US-10-186-042-7
; Sequence 7, Application US/10186042
; Patent No. 6642044
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7
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Query Match 100.0%; Score 40; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147
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RESULT 11
US-09-248-796A-22820
; Sequence 22820, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
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;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: US 60/096,409
;; PRIOR FILING DATE: 1998-08-13
;; NUMBER OF SEQ ID NOS: 28208
;; SEQ ID NO 22820
;; LENGTH: 180
;; TYPE: PRT
;; ORGANISM: Candida albicans
US-09-248-796A-22820

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Best Local Similarity 83.3%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQDYFH 7
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DB 102 NQDYFH 107

RESULT 12
US-09-583-110-4016
; Sequence 4016, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4016
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4016

Query Match 80.0%; Score 32; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDYFH 7
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DB 40 QDYFH 44

RESULT 13
US-09-107-433-4442
; Sequence 4442, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>

;; SOFTWARE: <Unknown>
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/107,433
;; FILING DATE: 30-Jun-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/ 085131
;; FILING DATE: May 12, 1998
;; APPLICATION NUMBER: 60/051553
;; FILING DATE: July 2, 1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ariniello, Pamela Deneke
;; REGISTRATION NUMBER: 40,489
;; REFERENCE/DOCKET NUMBER: GTC-011
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (781)893-5007
;; TELEFAX: (781)893-8277
;; INFORMATION FOR SEQ ID NO: 4442:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 95 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: YES
;; ORIGINAL SOURCE:
;; ORGANISM: Streptococcus pneumoniae
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (B) LOCATION 1...95
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4442:
US-09-107-433-4442

Query Match 80.0%; Score 32; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDYFH 7
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DB 51 QDYFH 55

RESULT 14
US-08-700-359-21
; Sequence 21, Application US/08700359
; Patent No. 5766925
; GENERAL INFORMATION:
; APPLICANT: SUGIMOTO, MASAKAZU
; APPLICANT: USUDA, YOSHIHIRO
; APPLICANT: SUZUKI, TOMOKO
; APPLICANT: TANAKA, AKIKO
; APPLICANT: MATSUI, HIROSHI
; TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS TEXT EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,359
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-35019
; FILING DATE: 04-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: NORMAN F. OBLON

REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-819-0 PCT
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-700-359-21

Query Match 80.0%; Score 32; DB 1; Length 369;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 133 SSMDYFH 139

RESULT 15
US-08-616-392C-4
Sequence 4, Application US/08616392C
Patent No. 5998165
GENERAL INFORMATION:
APPLICANT: Goold, Richard D.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Seilhamer, Jeffrey
APPLICANT: Coleman, Roger
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES PANCLIA
TITLE OF INVENTION: AND PANCLB ASSOCIATED WITH PANCREATIC CANCER
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/616,392C
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/581,240
FILING DATE: 29-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0052-IUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: hnt
CLONE: 496071
US-08-616-392C-4

Query Match 80.0%; Score 32; DB 2; Length 583;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 433 STDDYFH 439

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Job time : 2.05405 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:11:05 ; Search time 3.7973 Seconds
(without alignments)
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Title: US-10-820-200-2_COPY_161_167
Perfect score: 40
Sequence: 1 SSQDYFH 7

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	476	17 US-10-877-849-43	Sequence 43, Appl
2	40	100.0	478	14 US-10-184-771-10	Sequence 10, Appl
3	40	100.0	478	14 US-10-186-042-7	Sequence 7, Appl
4	40	100.0	478	15 US-10-644-187-7	Sequence 7, Appl
5	40	100.0	478	17 US-10-926-720-10	Sequence 10, Appl
6	40	100.0	478	17 US-10-980-759-7	Sequence 7, Appl
7	40	100.0	478	20 US-11-064-196-10	Sequence 10, Appl
8	40	100.0	498	16 US-10-815-495-22	Sequence 22, Appl
9	40	100.0	498	16 US-10-820-200-2	Sequence 2, Appl
10	40	100.0	498	17 US-10-877-849-30	Sequence 30, Appl
11	40	100.0	499	16 US-10-815-495-18	Sequence 18, Appl

12	40	100.0	499	16	US-10-797-393A-5	Sequence 5, Appl
13	40	100.0	608	17	US-10-877-849-40	Sequence 40, Appl
14	40	100.0	640	17	US-10-877-849-36	Sequence 36, Appl
15	40	100.0	1095	14	US-10-228-063-45	Sequence 45, Appl
16	34	85.0	256	14	US-10-298-638-16	Sequence 16, Appl
17	33	82.5	133	15	US-10-424-599-175172	Sequence 175172, Appl
18	33	82.5	133	15	US-10-424-599-218859	Sequence 218859, Appl
19	33	82.5	167	16	US-10-767-701-39199	Sequence 39199, A
20	33	82.5	193	16	US-10-437-963-140941	Sequence 140941, A
21	33	82.5	697	16	US-10-425-115-275630	Sequence 275630, A
22	33	82.5	703	15	US-10-425-114-65668	Sequence 65668, A
23	33	82.5	1731	17	US-10-732-923-8855	Sequence 8855, Ap
24	33	82.5	3124	17	US-10-732-923-8854	Sequence 8854, Ap
25	33	82.5	4351	10	US-09-970-944-20	Sequence 20, Appl
26	32	80.0	71	15	US-10-424-599-162174	Sequence 162174, A
27	32	80.0	79	16	US-10-425-115-187129	Sequence 187129, A
28	32	80.0	86	16	US-10-425-115-355307	Sequence 355307, A
29	32	80.0	95	18	US-10-617-320-4442	Sequence 4442, Ap
30	32	80.0	119	15	US-10-264-049-4124	Sequence 4124, Ap
31	32	80.0	152	16	US-10-425-115-271310	Sequence 271310, A
32	32	80.0	180	17	US-10-472-928-496	Sequence 496, App
33	32	80.0	323	15	US-10-282-122A-72639	Sequence 72639, A
34	32	80.0	501	18	US-10-450-763-45485	Sequence 45485, A
35	32	80.0	529	20	US-11-097-143-39465	Sequence 39465, A
36	32	80.0	583	9	US-09-924-654-4	Sequence 4, Appl
37	32	80.0	594	9	US-09-925-300-1079	Sequence 1079, Ap
38	32	80.0	820	15	US-10-369-493-686	Sequence 686, App
39	32	80.0	820	15	US-10-282-122A-42805	Sequence 42805, A
40	32	80.0	820	15	US-10-282-122A-74838	Sequence 74838, A
41	32	80.0	820	15	US-10-282-122A-75391	Sequence 75391, A
42	32	80.0	820	15	US-10-272-107-3	Sequence 3, Appl
43	32	80.0	820	17	US-10-689-395-3	Sequence 3, Appl
44	32	80.0	885	16	US-10-437-963-136212	Sequence 136212, A
45	32	80.0	1118	14	US-10-153-668-104	Sequence 104, App

ALIGNMENTS

RESULT 1
US-10-877-849-43
; Sequence 43, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877, 849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 43
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)..(476)
US-10-877-849-43

Query Match 100.0%; Score 40; DB 17; Length 476;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

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RESULT 2
US-10-184-771-10
; Sequence 10, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1f216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-10-184-771-10

Query Match          100.0%; Score 40; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 3
US-10-186-042-7
; Sequence 7, Application US/10186042
; Publication No. US20030171236A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match          100.0%; Score 40; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 4
US-10-644-187-7
; Sequence 7, Application US/10644187
; Publication No. US20040048351A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/644,187
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-644-187-7

Query Match          100.0%; Score 40; DB 15; Length 478;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 5
US-10-926-720-10
; Sequence 10, Application US/10926720
; Publication No. US20050019886A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/926,720
; FILING DATE: 26-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
```

REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10

Query Match 100.0%; Score 40; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 6

US-10-980-759-7
; Sequence 7, Application US/10980759
; Publication No. US20050118695A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/980,759
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-980-759-7

Query Match 100.0%; Score 40; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 7

US-11-064-196-10
; Sequence 10, Application US/11064196
; Publication No. US20050170487A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants

FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/11/064,196
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-11-064-196-10

Query Match 100.0%; Score 40; DB 20; Length 478;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 8

US-10-815-495-22
; Sequence 22, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connelly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; TITLE OF INVENTION: Mutants Of Aspergillus Niger
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-22

Query Match 100.0%; Score 40; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 9

US-10-820-200-2
; Sequence 2, Application US/10820200
; Publication No. US20040229764A1
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Pedersen, Sven
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
; FILE REFERENCE: 5835.200-US
; CURRENT APPLICATION NUMBER: US/10/820,200
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US/09/710,339
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/165,786
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2

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; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus Oryzae
US-10-820-200-2

Query Match      100.0%; Score 40; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSQDYFH 7
      |||||
Db      161 SSQDYFH 167

RESULT 10
US-10-877-849-30
; Sequence 30, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-877-849-30

Query Match      100.0%; Score 40; DB 17; Length 498;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSQDYFH 7
      |||||
Db      161 SSQDYFH 167

RESULT 11
US-10-815-495-18
; Sequence 18, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connelly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; TITLE OF INVENTION: Mutants Of Aspergillus Niger
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-18

Query Match      100.0%; Score 40; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSQDYFH 7
      |||||
```

```
Db      162 SSQDYFH 168

RESULT 12
US-10-797-393A-5
; Sequence 5, Application US/10797393A
; Publication No. US20040219649A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Hans Sejr
; APPLICANT: Pedersen, Sven
; APPLICANT: Festeren, Rikke Monica
; TITLE OF INVENTION: ALCOHOL PRODUCT PROCESSES
; FILE REFERENCE: 10391.200-US
; CURRENT APPLICATION NUMBER: US/10/797,393A
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-797-393A-5

Query Match      100.0%; Score 40; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSQDYFH 7
      |||||
Db      162 SSQDYFH 168

RESULT 13
US-10-877-849-40
; Sequence 40, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-40

Query Match      100.0%; Score 40; DB 17; Length 608;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSQDYFH 7
      |||||
Db      161 SSQDYFH 167

RESULT 14
US-10-877-849-36
; Sequence 36, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
```

; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-36

Query Match 100.0%; Score 40; DB 17; Length 640;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
|||
Db 161 SSQDYFH 167

RESULT 15
US-10-228-063-45
; Sequence 45, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lananan, Mike
; TITLE OF INVENTION: Self-processing Plants and Plant Parts
; FILE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Aspergillus shirousami
US-10-228-063-45

Query Match 100.0%; Score 40; DB 14; Length 1095;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
|||
Db 141 SSQDYFH 147

Search completed: November 7, 2005, 18:45:04
Job time : 4.7973 secs

The Page Book (1900)

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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:58:55 ; Search time 4.02703 Seconds
(without alignments)
672.288 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167

Perfect score: 7

Sequence: 1 SSQDYFH 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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1: Genesepc19808:*
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3: Genesepc20008:*
4: Genesepc20018:*
5: Genesepc20028:*
6: Genesepc20038:*
7: Genesepc20038a:*
8: Genesepc20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	423	4 ABB09072	Abb09072 Aspergill
2	7	100.0	478	2 AAR46065	Aar46065 Mutant al
3	7	100.0	478	2 AAR72450	Aar72450 Aspergill
4	7	100.0	478	2 AAR78270	Aar78270 Aspergill
5	7	100.0	478	2 AAR79025	Aar79025 Mature ta
6	7	100.0	478	2 AAW14500	Aaw14500 Aspergill
7	7	100.0	498	4 AAB84206	Aab84206 Amino aci
8	7	100.0	498	8 ADT09632	Adt09632 Aspergill
9	7	100.0	499	8 ADT09628	Adt09628 Aspergill
10	7	100.0	1095	6 ABP96630	Abp96630 Alpha-amy
11	6	85.7	182	5 ABP28341	Abp28341 Streptoco
12	6	85.7	351	8 AD061605	Ad061605 Transcrip
13	6	85.7	493	2 AAR88212	Aar88212 Alpha-amy
14	5	71.4	45	4 AAM24481	Aam24481 Human EST
15	5	71.4	52	4 AAO08447	Aao08447 Human pol
16	5	71.4	61	4 AAO02433	Aao02433 Human pol
17	5	71.4	69	4 ABB15756	Abb15756 Human ner
18	5	71.4	84	8 ADK47501	Adk47501 Streptoco
19	5	71.4	88	4 ABB08450	Abb08450 Human pho
20	5	71.4	94	4 ABB71558	Abb71558 Drosophil
21	5	71.4	95	4 AAG64127	Aag64127 Human TNF
22	5	71.4	95	8 ADR95807	Adr95807 Novel S.
23	5	71.4	104	3 AAY90470	Aay90470 Yeast Sml
24	5	71.4	119	4 AAU31764	Aau31764 Novel hum
25	5	71.4	123	4 AAO08298	Aao08298 Human pol

26	5	71.4	128	5 ABB98330	Abb98330 Subtilisi
27	5	71.4	131	4 AAO03876	Aao03876 Human pol
28	5	71.4	134	7 ADD19267	Add19267 Human sec
29	5	71.4	151	7 ADK52505	Adk52505 Penicilli
30	5	71.4	154	2 AAY30848	Aay30848 Human sec
31	5	71.4	180	6 ABU00681	Abu00681 S. pneumo
32	5	71.4	180	8 ADM92084	Adm92084 S. pneumo
33	5	71.4	185	5 ABP26186	Abp26186 Streptoco
34	5	71.4	189	6 ABP76858	Abp76858 N. gonorr
35	5	71.4	189	6 ABP78080	Abp78080 N. gonorr
36	5	71.4	222	4 AAU31887	Aau31887 Novel hum
37	5	71.4	222	8 ADQ66002	Adq66002 Novel hum
38	5	71.4	255	3 AAG33176	Aag33176 Zea may
39	5	71.4	280	3 AAG33175	Aag33175 Zea may
40	5	71.4	286	3 AAG33174	Aag33174 Zea may
41	5	71.4	298	6 ABUL6660	Abul6660 Protein e
42	5	71.4	303	6 ADA33877	Ada33877 Acinetoba
43	5	71.4	317	7 ADC95026	Adc95026 E. faeciu
44	5	71.4	326	6 ABP98616	Abp98616 Mature Br
45	5	71.4	330	4 AAB96495	Aab96495 Putative

ALIGNMENTS

RESULT 1

ABB09072
ID ABB09072 standard; protein; 423 AA.
XX
AC ABB09072;
XX
DT 26-JUN-2002 (first entry)
XX
DE Aspergillus oryzae TAKA protein (TAA).
XX
KW Thermus sp. IM6501; maltogenic amylase; EC 3.2.1.133; crystallisation;
KW protein co-ordinate data; 3 dimensional structure.
XX
OS Aspergillus oryzae.
XX
PN KR2001027418-A.
XX
PD 06-APR-2001.
XX
PF 09-SEP-1999; 99KR-00039130.
XX
PR 09-SEP-1999; 99KR-00039130.
XX
PA (POST-) POSTECH FOUND.
PA (SAMY-) SAMYANG GENEX CORP.
PI Kim TJ, Park GH;
DR WPI; 2001-534477/59.
XX
PT Manufacturing maltogenic amylase having improved transglycosylation
PT activity, comprises using crystallization.
XX
PS Disclosure; Page 188; 196pp; Korean.

XX
CC The present invention describes manufacturing maltogenic amylase (EC
CC 3.2.1.133) having improved transglycosylation activity, comprising using
CC crystallisation and the three dimensional structure of maltogenic
CC amylase. Manufacturing maltogenic amylase comprises the following steps:
CC (i) obtaining a gene of maltogenic amylase from Thermus sp. IM6501 (KCTC
CC 5027BP) and inserting the gene into plasmid pUC19 to construct
CC recombinant DNA (pTHM119); (ii) inserting the recombinant DNA to
CC Escherichia coli MC1061, which is cultivated at 37 plus degrees Celsius
CC for 10 hours in Luria-Bertani (LB) media and centrifuging the media to
CC obtain a microbial cell; (iii) suspending the microbial cell with buffer
CC solution at pH 7.5 and obtaining supernatant; and (iv) passing the
CC supernatant through column chromatography and obtaining purified of
CC maltogenic amylase. The maltogenic amylase is a dimer comprised of two

CC maltogenic amylase molecules, and a Thermus sp. IM6501 maltogenic amylase
 CC (ThMA) crystal. The amylase has a structure containing an activated
 CC region that consists of amino acid residues of Asp-328, Glu-357, Asp-424,
 CC and a pocket with glucose bound that consists of amino acid residues of
 CC Pro44, Tyr45, Arg81, Arg83, Prol18, Cys116, Asn131, Glu132, Val1329,
 CC and His1360. The present sequence represents Aspergillus oryzae TAKA
 CC protein (TAA), given in comparison with ThMA in the present invention
 XX
 SQ Sequence 423 AA;

Query Match 100.0%; Score 7; DB 4; Length 423;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||
 Db 137 SSQDYFH 143

RESULT 2
 AAR46065
 ID AAR46065 standard; protein; 478 AA.

XX AC AAR46065;
 XX DT 25-MAR-2003 (revised)
 XX DT 18-JUL-1994 (first entry)
 XX DE Mutant alpha-amylase.
 XX DE Methionine substitution; stability; activity; detergent;
 KW dishwashing agents; liquefaction agents.
 XX OS Aspergillus oryzae.

XX PN WO9402597-A1.
 XX PD 03-FEB-1994.

XX PF 06-JUL-1993; 93WO-DK000230.
 XX PR 23-JUL-1992; 92DK-00000946.
 XX PR 16-DEC-1992; 92DK-00001503.
 XX PR 15-MAR-1993; 93DK-00000292.

XX PA (NOVO) NOVO-NORDISK AS.
 XX PI Svendsen A, Bisgard-Frantzen H;
 XX WPI; 1994-048855/06.

XX DR Claim 1; Page 7; 20pp; English.
 XX PT Mutant alpha-amylase from Bacillus species comprising a methionine
 PT substitution - with improved stability and activity at low pH, for use in
 PT detergents, dishwashing agents and liquefaction agents.
 XX

XX CC The sequence os that of the Aspergillus oryzae alpha amylase, sold
 CC commercially as FUNGAMYL (TM) by Novo Nordisk A/S. The sequence can be
 CC mutated by substitution of one or more of its methionine residues for any
 CC amino acid other than cysteine. The mutant alpha-amylase exhibits a
 CC better activity level and better stability in the presence of oxidising
 CC agents than previous mutant alpha amylases, and improved thermostability
 CC at moderately low pH. The enzyme can be used as an additive for
 CC detergents, dishwashing agents and liquefaction agents. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX SQ Sequence 478 AA;

Query Match 100.0%; Score 7; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||
 Db 141 SSQDYFH 147
 RESULT 3
 AAR72450
 ID AAR72450 standard; protein; 478 AA.

XX AC AAR72450;
 XX DT 25-MAR-2003 (revised)
 XX DT 01-DEC-1995 (first entry)

XX DE Aspergillus oryzae alpha amylase (mature protein).

XX KW Alpha amylase; variant; enzyme; detergent; additive; dishwashing;
 KW washing; Bacillus licheniformis; Bacillus amyloliquefaciens;
 KW Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
 KW thermostable.

XX OS Aspergillus oryzae.
 XX PN WO9510603-A1.
 XX PD 20-APR-1995.

XX PF 05-OCT-1994; 94WO-DK000370.
 XX PR 08-OCT-1993; 93DK-00001133.
 XX PR 02-FEB-1994; 94DK-00000140.

XX PA (NOVO) NOVO-NORDISK AS.
 XX PI Borchert TV, Bisgard-Frantzen H, Svendsen A, Thellersen M;
 XX PI Van Der Zee P;
 XX WPI; 1995-161790/21.

XX PT New Bacillus derived alpha-amylase variants - having amino acid
 PT modifications to improve washing and/or dishwashing performance.
 XX PS Disclosure; Page 75-76; 105pp; English.

XX CC Variant alpha amylase enzymes which have improved washing and/or as
 CC detergent additives. The enzymes have one or more amino acid residues
 CC added, deleted or substituted. The variants can also be used for textile
 CC desizing prior to scouring, bleaching and dyeing. The variants have
 CC improved thermostability, acid/alkaline stability; low temperature
 CC optimum; pH optimum; higher hydrolysis velocity and improved tolerance to
 CC other composition constituents, e.g. oxidation agents. (Updated on 25-MAR
 CC -2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX SQ Sequence 478 AA;

Query Match 100.0%; Score 7; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||
 Db 141 SSQDYFH 147

RESULT 4
 AAR78270
 ID AAR78270 standard; protein; 478 AA.

XX AC AAR78270;
 XX DT 17-JAN-1996 (first entry)

XX DE Aspergillus oryzae alpha amylase (mature protein).

FT to 12-19 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 30"
FT
FT Misc-difference 32. .38
FT /label= loop 1 modification region
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 14-15 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 32"
FT
FT Misc-difference 66. .84
FT /label= loop 2 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 44-57 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 18"
FT
FT Misc-difference 70. .78
FT /label= loop 2 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 48-51 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 20"
FT
FT Misc-difference 98. .210
FT /label= loop 3 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 117-185 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 24"
FT
FT Misc-difference 102. .206
FT /label= loop 3 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 121-181 of AAW14499 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 26"
FT
FT Misc-difference 121. .181
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to this fragment is deleted or replaced with a fragment
FT corresponding to 102-206 of AAW14499; claim 41"
FT
FT Misc-difference 121. .174
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to this fragment is deleted or
FT replaced with a fragment corresponding to 102-199 of
FT AAW14499; claim 42"
FT
FT Misc-difference 165. .177
FT /label= loop 3 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 195-202 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 21"
FT
FT Misc-difference 166. .173
FT /label= loop 3 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 196-198 of AAW14499 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 23"
FT
FT Misc-difference 181. .184
FT /note= "an amino acid fragment corresponding to this
FT region is deleted from the parent sequence of a variant
FT Fungamyl; claim 43"
FT
FT Misc-difference 291. .313
FT /label= loop 8 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 322-346 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 36"
FT
FT Misc-difference 297. .313
FT /label= loop 8 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for

FT a variant) corresponding to 325-345 of AAW14498 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 38"
FT
FT WO9623874-A1.
FT
FT 08-AUG-1996.
FT
FT 05-FEB-1996; 96WO-DK000057.
FT
FT 03-FEB-1995; 95DK-0000128.
FT
FT 23-OCT-1995; 95DK-00001192.
FT
FT 10-NOV-1995; 95DK-00001256.
FT
FT (NOVO) NOVO-NORDISK AS.
FT
FT Svendsen A, Bisgard-Frantzen H, Borchert TV;
FT WPI; 1996-371424/37.
FT
FT Alpha-amylase variants and methods of production - have altered
FT properties such as calcium dependency, substrate binding and stability.
FT
FT Disclosure; Page 87-88; 171pp; English.
FT
FT The present sequence is the mature Aspergillus oryzae alpha-amylase (A).
FT Variants of parent termamyl- and fungamyl-like alpha-amylases (and
FT methods of constructing them) are claimed. Examples of variants are
FT featured above. The variants have altered properties such as: calcium
FT dependency, substrate binding and stability. Also one or more proline or
FT cysteine residues in the variant is modified or replaced with a non-
FT proline or non-cysteine residue such as alanine. The variants can be used
FT for (dish)washing, as detergent additives or for fabric desizing or
FT starch liquerfaction. They can also be used for the production of
FT sweeteners and ethanol from starch. See also AAW14498-99
FT
FT Sequence 478 AA;
FT
FT Query Match 100.0%; Score 7; DB 2; Length 478;
FT Best Local Similarity 100.0%; Pred. No. 2.1;
FT Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT
FT QY 1 SSQDYFH 7
FT |||||
FT Db 141 SSQDYFH 147
FT
FT RESULT 7
FT AAB84206
FT ID AAB84206 standard; protein; 498 AA.
FT
FT AC AAB84206;
FT
FT DT 06-AUG-2001 (first entry)
FT
FT DE Amino acid sequence of a fungamyl-like alpha-amylase.
FT
FT KW Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose;
FT alcohol; starch; dough improver; brewing; starch liquification.
FT
FT OS Aspergillus oryzae.
FT
FT FN WO200134784-A1.
FT
FT PD 17-MAY-2001.
FT
FT PF 10-NOV-2000; 2000WO-DK000626.
FT
FT PR 10-NOV-1999; 99DK-00001617.
FT
FT PA (NOVO) NOVOZYMES AS.
FT
FT Bisgard-Frantzen H, Svendsen A, Pedersen S;
FT

XX WPI; 2001-367478/38.
DR N-PSDB; AAF90208.
XX
PT New variant of Fungamyl-like alpha-amylase, useful for production of
PT maltose syrups, includes mutations that improve stability against heat
PT and acidic pH.
XX
PS Claim 1; Page 42-45; 49pp; English.
XX
XX The present sequence represents a fungamyl-like alpha-amylase. The
CC specification describes variants of this fungamyl-like alpha-amylase,
CC which have an alteration in one the amino acid regions 98-110, 150-160,
CC 161-167, 280-288, 448-455, and 468-475. Each alteration is a deletion or
CC substitution of an amino acid or an insertion of an amino acid downstream
CC of a particular position. The variants retain alpha-amylase activity, and
CC have better heat stability and/or stability at acidic pH, relative to
CC wild-type enzyme. The variants can therefore be used at higher
CC temperatures (more efficient conversion or faster reaction, and have
CC reduced need for cooling and reduced risk of contamination). The variants
CC may also be used in conjunction with other enzymes, particularly
CC glucoamylase during dextrinisation. The variants are used to produce
CC syrups, particularly of high maltose content, or alcohol, from starch; as
CC dough improver for baked goods; in brewing, to increase fermentability of
CC the wort; and for liquefaction of starch
XX
SQ Sequence 498 AA;
Query Match 100.0%; Score 7; DB 4; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
DB 161 SSQDYFH 167
|||||||
RESULT 8
ADT89632
ID ADT89632 standard; protein; 498 AA.
XX
AC ADT89632;
XX
DT 16-DEC-2004 (first entry)
XX
DE Aspergillus niger neutral alpha-amylase A (amyA) protein.
XX
KW Glucoamylase; glaA; amyA; alpha-amylase A; enzyme.
XX
OS Aspergillus niger.
XX
PN US2004191864-A1.
XX
PD 30-SEP-2004.
XX
PF 31-MAR-2004; 2004US-00815495.
XX
PR 31-MAR-2003; 2003US-0459902P.
XX
PA (NOVO) NOVOZYMES BIOTECH INC.
XX
PI Connelly M, Brody H;
XX
DR WPI; 2004-708545/69.
XX
PT N-PSDB; ADT89631.
XX
PT Producing heterologous biological substance comprises culturing mutant of
PT wild-type Aspergillus niger strain in medium suitable for producing
PT heterologous biological substance and recovering heterologous biological
PT substance.
XX
XX Example 11; SEQ ID NO 22; 59pp; English.

CC The present invention relates to a method of producing heterologous
CC biological substance. The method involves culturing mutant of wild-type
CC Aspergillus niger strain in medium suitable for producing heterologous
CC biological substance, where mutant strain comprises first nucleotide
CC sequence encoding heterologous biological substance and second nucleotide
CC sequences comprising modification of glucoamylase (glaA) and recovering
CC heterologous biological substance. The present sequence is the
CC Aspergillus niger neutral alpha-amylase A (amyA) protein.
XX
SQ Sequence 498 AA;
Query Match 100.0%; Score 7; DB 8; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
DB 162 SSQDYFH 168
|||||||
RESULT 9
ADT89628
ID ADT89628 standard; protein; 499 AA.
XX
AC ADT89628;
XX
DT 16-DEC-2004 (first entry)
XX
DE Aspergillus niger neutral alpha-amylase B (amyB) protein.
XX
KW Glucoamylase; glaA; amyB; alpha-amylase B; enzyme.
XX
OS Aspergillus niger.
XX
PN US2004191864-A1.
XX
PD 30-SEP-2004.
XX
PF 31-MAR-2004; 2004US-00815495.
XX
PR 31-MAR-2003; 2003US-0459902P.
XX
PA (NOVO) NOVOZYMES BIOTECH INC.
XX
PI Connelly M, Brody H;
XX
DR WPI; 2004-708545/69.
XX
PT N-PSDB; ADT89627.
XX
PT Producing heterologous biological substance comprises culturing mutant of
PT wild-type Aspergillus niger strain in medium suitable for producing
PT heterologous biological substance and recovering heterologous biological
PT substance.
XX
XX Example 10; SEQ ID NO 18; 58pp; English.
XX
XX The present invention relates to a method of producing heterologous
CC biological substance. The method involves culturing mutant of wild-type
CC Aspergillus niger strain in medium suitable for producing heterologous
CC biological substance, where mutant strain comprises first nucleotide
CC sequence encoding heterologous biological substance and second nucleotide
CC sequences comprising modification of glucoamylase (glaA) and recovering
CC heterologous biological substance. The present sequence is the
CC Aspergillus niger neutral alpha-amylase B (amyB) protein.
XX
SQ Sequence 499 AA;
Query Match 100.0%; Score 7; DB 8; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
|||||||

```

Db      162 SSQDYFH 168

RESULT 10
ABP96630
ID ABP96630 standard; protein; 1095 AA.
XX
AC ABP96630;
XX
DT 02-JUN-2003 (first entry)
XX
DE Alpha-amylase/glucosylase fusion protein sequence SEQ ID NO:45.
XX
KW Self-processing plant; plant; processing enzyme; alpha-amylase; grain;
KW pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase;
KW mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch;
KW maltodextrin; ethanol; fermentation; beverage; enzyme.
XX
OS Aspergillus shirousami.
XX Synthetic.
XX
PN WO2003018766-A2.
XX
PD 06-MAR-2003.
XX
PF 27-AUG-2002; 2002WO-US027129.
XX
PR 27-AUG-2001; 2001US-0315281P.
XX
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI Lanahan MB, Basu SS, Batie CJ, Chen W, Craig J, Kinkema M;
XX
DR WPI: 2003-268420/26.
XX N-PSDB; ACC44572.
XX
PT Novel polynucleotide encoding hyperthermophilic processing enzymes e.g.
PT alpha-amylase, useful for producing plant to produce food products having
PT improved taste or fermentable substrates for ethanol.
XX
PS Claim 1; Page 107; 158pp; English.
XX
CC The present invention describes polynucleotides which encode processing
CC enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose
CC isomerase, or glucoamylase) that are optimised for expression in plants.
CC The polynucleotides encode mesophilic, thermophilic or hyperthermophilic
CC processing enzymes, which are activated under suitable conditions to act
CC upon the desired substrate. Also described are self-processing transgenic
CC plants and plant parts, e.g. grain, which express one or more of these
CC enzymes and have an altered composition that facilitates plant and grain
CC processing. Also described is a method (M) for converting starch to
CC starch-derived products in a transformed plant part (Tpp), by activating
CC the starch processing enzyme contained in it. Transgenic grain is useful
CC for preparing maltodextrin. A transformed plant (Tp) can be used to
CC produce food products having improved taste and to produce fermentable
CC substrates for ethanol and fermented beverages. (M) eliminates the need
CC to mill or physically disrupt the integrity of plant parts prior to
CC recovery of starch-derived products. The present sequence represents
CC alpha-amylase/glucoamylase fusion protein, which is given in the
CC exemplification of the present invention
XX
SQ Sequence 1095 AA;
Query Match 100.0%; Score 7; DB 6; Length 1095;
Best Local Similarity 100.0%; Pred. No. 4.2; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 11

ABP28341
ID ABP28341 standard; protein; 182 AA.
XX
AC ABP28341;
XX
DT 02-JUL-2002 (first entry)
XX
DE Streptococcus polypeptide SEQ ID NO 5858.
XX
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX
OS Streptococcus agalactiae.
XX
PN WO200234771-A2.
XX
PD 02-MAY-2002.
XX
PF 29-OCT-2001; 2001WO-GB004789.
XX
PR 27-OCT-2000; 2000GB-00026333.
XX 24-NOV-2000; 2000GB-00028727.
XX 07-MAR-2001; 2001GB-00005640.
XX
PA (CHIR-) CHIRON SPA.
XX (GENO-) INST GENOMIC RES.
XX
PI Telford J, Masignani V, Margarit Y RosI, Grandi G, Fraser C;
PI Tettelin H;
XX
DR WPI: 2002-352536/38.
XX N-PSDB; ABN68972.
XX
PT New Streptococcus protein for the treatment or prevention of infection or
PT disease caused by Streptococcus bacteria, such as meningitis, and for
PT detecting a compound that binds to the protein.
XX
PS Claim 1; Page 3748; 4525pp; English.
XX
CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins
XX
SQ Sequence 182 AA;
Query Match 85.7%; Score 6; DB 5; Length 182;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYF 6
Db 134 SSQDYF 139

RESULT 12
AD061605
ID AD061605 standard; protein; 351 AA.
XX

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AC ADO61605;
XX
DT 15-JUL-2004 (first entry)
XX
DE Transcription factor G319, SEQ ID 72.
XX
DE Plant; transcription factor; transgenic plant; abiotic stress tolerance;
KW osmotic stress tolerance; cold tolerance; heat tolerance;
KW low nitrogen tolerance; low phosphate tolerance; fungal disease;
KW glyphosate resistance; flowering; fertility; seed development.
XX
XX Arabidopsis thaliana.
XX
XX WO2004031349-A2.
XX
XX 15-APR-2004.
XX
XX 18-SEP-2003; 2003WO-US030292.
XX
XX 18-SEP-2002; 2002US-0411837P.
XX
XX 17-DEC-2002; 2002US-0434166P.
XX
XX 24-APR-2003; 2003US-0465809P.
XX
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
XX
XX Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;
PI Riechmann JU, Haake V, Dubell AN, Keddle JS, Sherman BK;
XX
XX WPI; 2004-330163/30.
XX
XX N-PSDB; ADO61604.
XX
XX New recombinant polynucleotide encoding transcription factor
PT polypeptides, useful for producing transgenic plants with advantageous
PT properties compared to a reference plant.
XX
XX Claim 16; SEQ ID NO 72; 510pp; English.
XX
XX The present invention relates to novel plant transcription factor
CC proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The
CC sequences can be used to produce transgenic plants, which overexpress
CC (II), where the transgenic plant has an altered trait as compared to a
CC non-transgenic plant or wild-type plant. The transgenic plant comprises
CC an altered trait selected from increased tolerance to abiotic stress,
CC increased tolerance to osmotic stress, increased tolerance to cold,
CC increased germination in cold, increased tolerance to heat, increased
CC germination in heat, increased tolerance to freezing conditions,
CC increased tolerance to low nitrogen conditions, increased tolerance to
CC low phosphate conditions, increased tolerance to disease, including
CC fungal disease and particularly Erysiphe, Fusarium and Botrytis,
CC increased tolerance to multiple fungal pathogens, increased resistance to
CC glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,
CC increased sensitivity to ACC, altered sugar sensing, increased tolerance
CC to sugars, altered carbon/nitrogen sensing, early flowering, late
CC flowering, altered flower structure, loss of flower determinacy, reduced
CC fertility, altered shoot meristem development, altered branching pattern,
CC altered stem morphology, altered vascular tissue structure, reduced
CC apical dominance, altered trichome density, altered trichome development,
CC altered trichome structure, altered root development, altered shade
CC avoidance, altered seed development, altered seed ripening, altered seed
CC germination, slow growth, fast growth, altered cell differentiation,
CC altered cell proliferation, altered cell expansion, altered phase change,
CC altered senescence, abnormal embryo development, altered programmed cell
CC death, lethality when overexpressed, altered necrosis patterns, increased
CC plant size, increased biomass, large seedlings, dwarfed plants, dark
CC green leaves, change in leaf shape, increased leaf size and mass, light
CC green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,
CC altered seed coloration, altered seed size, altered seed shape, large
CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil
CC content, altered seed protein content, altered seedprenyl content,
CC altered leaf prenyl lipid content, increased anthocyanin levels, and
CC decreased anthocyanin levels. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 351 AA;
XX
Query Match 85.7%; Score 6; DB 8; Length 351;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYF 6
DB 226 SSQDYF 231
XX
RESULT 13
AAR88212
ID AAR88212 standard; protein; 493 AA.
XX
XX AAR88212;
AC
XX 16-OCT-2003 (revised)
DT 03-APR-1996 (first entry)
XX
XX Alpha-amylase.
DE
XX Alpha-amylase; thermostable enzyme; baking; Aspergillus niger.
KW
XX Thermomyces lanuginosus; CBS 224.63.
OS
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT /label= Sig_peptide
XX
XX WO9601323-A1.
PN
XX 18-JAN-1996.
PD
XX 03-JUL-1995; 95WO-EP002607.
PF
XX 04-JUL-1994; 94GB-00013419.
PR
XX (DANI-) DANISCO AS.
PA
XX Michelsen B, Rasmussen P;
PI
XX WPI; 1996-087673/09.
DR
XX N-PSDB; AAT10562.
XX
XX Thermophilic alpha-amylase with activity range of 60-80 degrees C -
PT derived from Thermomyces lanuginosus, useful in the prepn. of foodstuffs
PT and bakery prods. esp. bread.
XX
XX Claim 3; Page 36-38; 94pp; English.
XX
XX A thermostable alpha-amylase (AAR88212) of Thermomyces lanuginosus CBS
CC 224.63 is expressed in Aspergillus niger hosts using a gene (AAT10562)
CC isolated from a T. lanuginosus gene library. The recombinant enzyme (54-
CC 60 kDa) shows optimal activity at 60-70 deg and pH 5.8-6, has a pI of 3.7
CC and is active at 60-80 deg. (Updated on 16-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 493 AA;
XX
Query Match 85.7%; Score 6; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SQDYFH 7
DB 162 SQDYFH 167
XX
RESULT 14
AAW24481

ID AAM24481 standard; protein; 45 AA.
XX AC AAM24481;
XX DT 12-OCT-2001 (first entry)
XX DE Human EST encoded protein SEQ ID NO: 2006.
XX KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition.
XX OS Homo sapiens.
XX PN WO200154477-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US002687.
XX PR 25-JAN-2000; 2000US-00491404.
XX PR 17-JUL-2000; 2000US-00617746.
XX PR 03-AUG-2000; 2000US-00631451.
XX PR 15-SEP-2000; 2000US-00663870.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX DR WPI; 2001-476164/51.
XX DR N-PSDB; AAH99140.
XX PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX PS Claim 20; Page 1269; 1275pp; English.
XX CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention
XX SQ Sequence 45 AA;
Query Match 71.4%; Score 5; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SQDYF 6
DB 22 SQDYF 26
RESULT 15
AAO08447
ID AAO08447 standard; protein; 52 AA.
XX AC AAO08447;
XX DT 06-NOV-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 22339.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.

XX OS Homo sapiens.
XX PN WO200164835-A2.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-US004927.
XX PR 28-FEB-2000; 2000US-00515126.
XX PR 18-MAY-2000; 2000US-00577409.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI; 2001-514838/56.
XX DR N-PSDB; AA188378.
XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX PS Claim 20; SEQ ID NO 22339; 1399pp + Sequence Listing; English.
XX CC The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 52 AA;
Query Match 71.4%; Score 5; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDY 5
DB 2 SSQDY 6

Search completed: November 7, 2005, 19:27:58
Job time : 7.02703 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2005, 19:15:40 ; Search time 0.851351 Seconds
(without alignments)
791.116 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167

Perfect score: 7

Sequence: 1 SSQDYFH 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	478	2 JK0201	alpha-amylase (EC
2	7	100.0	498	2 A48305	alpha-amylase (EC
3	7	100.0	499	1 ALAS1	alpha-amylase (EC
4	7	100.0	499	1 ALAS3	alpha-amylase (EC
5	7	100.0	499	2 JS0663	alpha-amylase (EC
6	7	100.0	499	2 JT0466	alpha-amylase (EC
7	7	100.0	499	2 JN0588	alpha-amylase (EC
8	7	100.0	499	2 B48305	alpha-amylase (EC
9	7	100.0	624	1 JC4510	pullulanase (EC 3.
10	6	85.7	317	2 E84088	restriction endonu
11	6	85.7	351	2 E86187	rup8h12.10 {import
12	5	71.4	104	2 S49803	hypothetical prote
13	5	71.4	129	2 H71046	hypothetical prote
14	5	71.4	144	2 JC7121	androgenic gland h
15	5	71.4	178	2 H96905	hypothetical prote
16	5	71.4	180	2 B95039	hypothetical prote
17	5	71.4	217	1 S61191	asymmetrical hydro
18	5	71.4	253	2 A05283	spectrin alpha cha
19	5	71.4	289	2 A43562	homeotic protein H
20	5	71.4	295	2 B84747	hypothetical prote
21	5	71.4	326	2 AF2082	iron(III) dicitrat
22	5	71.4	330	2 H75068	dipeptide abc tran
23	5	71.4	330	2 B71163	probable oligopept
24	5	71.4	331	2 T06227	peroxidase (EC 1.1
25	5	71.4	332	2 T10790	peroxidase (EC 1.1
26	5	71.4	420	2 T42616	envelope protein -
27	5	71.4	423	2 A12189	hypothetical prote
28	5	71.4	426	2 H71483	probable phosphat
29	5	71.4	459	2 H81324	probable MCP-domai

30	5	71.4	469	2 B90110	TATA box-binding p
31	5	71.4	482	2 A90248	conserved hypothet
32	5	71.4	486	2 AD0373	probable exported
33	5	71.4	547	2 S61032	hypothetical prote
34	5	71.4	551	1 JC5225	dsRNA-activated pr
35	5	71.4	569	2 C87598	TonB-dependent rec
36	5	71.4	569	2 B64646	polyposphate kina
37	5	71.4	675	2 F71935	polyposphate kina
38	5	71.4	813	2 I41292	EcOg type I restri
39	5	71.4	829	2 AC0776	probable outer mem
40	5	71.4	837	2 H87638	TonB-dependent rec
41	5	71.4	863	2 T47038	hypothetical prote
42	5	71.4	863	2 AD0234	probable fimbrial
43	5	71.4	943	2 T33795	hypothetical prote
44	5	71.4	1262	2 T30524	protein phosphatas
45	5	71.4	1564	2 S55517	probable transport

ALIGNMENTS

RESULT 1

JK0201

alpha-amylase (EC 3.2.1.1) - Aspergillus oryzae

N:Alternate names: glycogenase; Taka-amylase A

C:Species: Aspergillus oryzae

C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004

C:Accession: JK0201

R:Toda, H.; Kondo, K.; Narita, K.

Proc. Jpn. Acad. 58B, 208-212, 1982

A:Title: The complete amino acid sequence of Taka-amylase A.

A:Reference number: JK0201

A:Accession: JK0201

A:Molecule type: protein

A:Residues: 1-478 <TOD>

A:Cross-references: UNIPROT:P10529

C:Comment: One atom of calcium per molecule is essential for the activity.

C:Comment: This enzyme is a glycoprotein.

C:Comment: See also PIR:JT0466 and PIR:JS0240.

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F:173-300/Domain: alpha-amylase core homology <AMY>

F:197/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:210,230,297/Active site: His, Glu, Asp #status experimental

Query Match 100.0%; Score 7; DB 2; Length 478;

Best Local Similarity 100.0%; Pred. No. 0.33;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSQDYFH 7

|||||

Db 141 SSQDYFH 147

RESULT 2

A48305

alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori

C:Species: Aspergillus awamori

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C:Accession: A48305

R:Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;

Curr. Genet. 17, 203-212, 1990

A:Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe

A:Reference number: A48305; MUID:90254827; PMID:2340591

A:Accession: A48305

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-498 <KOR>

A:Cross-references: UNIPROT:Q02905

C:Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A;Pathway: glycogen/starch degradation
 C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
 C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
 F;194-321/Domain: alpha-amylase core homology <AMY>

Query Match 100.0%; Score 7; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 0.35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||
 Db 162 SSQDYFH 168

RESULT 3

ALAS1

Alpha-amylase (EC 3.2.1.1) 1 precursor [validated] - Aspergillus oryzae
 N;Alternate names: alpha-amylase isozyme II; glycogenase; Taka-amylase A
 C;Species: Aspergillus oryzae
 C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
 C;Accession: S04548; A33214; J50240; A91930; A93767; A10627
 R;Wirsal, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.

Mol. Microbiol. 3, 3-14, 1989

A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon c
 A;Reference number: S04548; MUID:89237897; PMID:2785629

A;Accession: S04548

A;Molecule type: DNA

A;Residues: 1-499 <WR>

A;Cross-references: UNIPROT:P10529; EMBL:X12725; NID:G2430; PIDN:CAA31218.1; PID:G295921

A;Genetics: AMY1

A;Accession: A33214

A;Molecule type: mRNA

A;Residues: 1-499 <WI2>

A;Cross-references: GB:X12725; NID:G2430; PIDN:CAA31218.1; PID:G295921

R;Genes, M.J.; Dove, M.J.; Seligy, V.L.

Gene 79, 107-117, 1989

A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing
 A;Reference number: JS0240; MUID:89378767; PMID:2789162

A;Accession: JS0240

A;Molecule type: DNA

A;Residues: 1-499 <GEN>

A;Genetics: AMY2

A;Note: the authors refer to this as isozyme II

R;Isemura, S.; Ikenaka, T.

J. Biochem. 74, 1-10, 1973

A;Reference number: A91930; MUID:74001521; PMID:4733850

A;Accession: A91930

A;Molecule type: protein

A;Residues: 206-225 <ISE>

R;Narita, K.

Proc. Jpn. Acad. 51, 285-290, 1975

A;Reference number: A93767

A;Accession: A93767

A;Molecule type: protein

A;Residues: 434-443, 446-447, 'Q', 449-458, 'GTTV', 459-464, 467-468, 'B', 470, 'B', 472-499 <NAR>

R;Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.

J. Biochem. 95, 697-702, 1984

A;Title: Structure and possible catalytic residues of Taka-amylase A.

A;Reference number: A37454; MUID:84212370; PMID:6609921

A;Contents: annotation; X-ray crystallography, 3.0 angstroms

R;Swift, H.J.; Brady, L.; Derewenda, Z.S.; Dodson, E.J.; Turkmenburg, J.P.; Wilkinson, A.
 submitted to the Brookhaven Protein Data Bank, August 1992

A;Reference number: A51548; PDB:6TAA

A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 22-497

C;Comment: One atom of calcium per molecule is essential for activity.

C;Genetics: <AMY1>

A;Gene: amy1

A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3

C;Genetics: <AMY2>

A;Gene: amy2; AmyII

A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A;Pathway: glycogen/starch degradation
 C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
 C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; poly
 F;1-21/Domain: signal sequence #status predicted <SIG>
 F;22-499/Product: alpha-amylase 1 #status experimental <MAT>
 F;194-321/Domain: alpha-amylase core homology <AMY>
 F;51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
 F;142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
 F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;227,251,318/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 7; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 0.35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||
 Db 162 SSQDYFH 168

RESULT 4

ALAS3

Alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae

N;Alternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A

C;Species: Aspergillus oryzae

C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004

C;Accession: S04549; A33215; A44713

R;Wirsal, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.

Mol. Microbiol. 3, 3-14, 1989

A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon c

A;Reference number: S04548; MUID:89237897; PMID:2785629

A;Accession: S04549

A;Molecule type: DNA

A;Residues: 1-499 <WR>

A;Cross-references: UNIPROT:Q96TH4; EMBL:X12727; NID:G2454; PIDN:CAA31220.1; PID:G295922

A;Accession: A33215

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-499 <WI2>

A;Cross-references: GB:X12727; NID:G2454; PIDN:CAA31220.1; PID:G295922

R;Genes, M.J.; Dove, M.J.; Seligy, V.L.

Gene 79, 107-117, 1989

A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing

A;Reference number: JS0240; MUID:89378767; PMID:2789162

A;Accession: A44713

A;Molecule type: DNA

A;Residues: 1-499 <GEN>

A;Note: the authors refer to this as isozyme I

R;Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.

J. Biochem. 95, 697-702, 1984

A;Title: Structure and possible catalytic residues of Taka-amylase A.

A;Reference number: A37454; MUID:84212370; PMID:6609921

A;Contents: annotation; X-ray crystallography, 3.0 angstroms

C;Comment: One atom of calcium per molecule is essential for activity.

C;Genetics:

A;Gene: amy3; AmyI

A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; metal

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-499/Product: alpha-amylase 3 #status experimental <MAT>

F;194-321/Domain: alpha-amylase core homology <AMY>

F;51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental

F;142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted

F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;231,251,318/Active site: His, Glu, Asp #status experimental

Query Match 100.0%; Score 7; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 0.35;


```

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 162 SSQDYFH 168

RESULT 5
JS0663
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus sp.
C:Species: Aspergillus sp.
C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
C:Accession: JS0663
R:Shibuya, I.; Tamura, G.; Ishikawa, T.; Hara, S.
Biosci. Biotechnol. Biochem. 56, 174-179, 1992
A:Title: Cloning of the alpha-amylase cDNA of Aspergillus shiroyamii and its expression
A:Reference number: JS0663; MUID:92323146; PMID:1368777
A:Accession: JS0663
A:Molecule type: mRNA
A:Residues: 1-499 <SHI>
A:Cross-references: UNIPROT:P10529
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-499/Product: alpha-amylase #status predicted <ALP>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 7; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 162 SSQDYFH 168

RESULT 6
JT0466
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N:Alternate names: glycogenase; taka-amylase A
C:Species: Aspergillus oryzae
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: JT0466
R:Tada, S.; Iimura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.
Agric. Biol. Chem. 53, 593-599, 1989
A:Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergillus
A:Reference number: JT0466
A:Accession: JT0466
A:Molecule type: DNA
A:Residues: 1-499 <TAD>
A:Cross-references: UNIPROT:P10529
C:Comment: See also PIR:JK0201 and PIR:JS0240.
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-499/Product: alpha-amylase #status predicted <MAT>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:231,251,318/Active site: His, Glu, Asp #status predicted

Query Match 100.0%; Score 7; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 SSQDYFH 7
DB 162 SSQDYFH 168

```

RESULT 7

```

JN0588
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N:Alternate names: Taka-amylase A
C:Species: Aspergillus oryzae
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: JN0588
R:Toukagoshi, N.; Furukawa, M.; Nagaba, H.; Kiritu, N.; Tsuboi, A.; Uda, S.
Gene 84, 319-327, 1989
A:Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for m
A:Reference number: JN0588; MUID:90128276; PMID:2612911
A:Accession: JN0588
A:Molecule type: mRNA
A:Residues: 1-499 <TSU>
A:Cross-references: UNIPROT:Q96TH4
C:Comment: The alpha amylases are encoded by multigene family.
C:Genetics:
A:Gene: Taa-G1
A:Introns: 56/1; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-499/Product: alpha-amylase #status predicted <MAT>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

```

Query Match 100.0%; Score 7; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 SSQDYFH 7
DB 162 SSQDYFH 168

```

RESULT 8

```

B48305
alpha-amylase (EC 3.2.1.1) B precursor - Aspergillus awamori
C:Species: Aspergillus awamori
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: B48305
R:Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A:Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe
A:Reference number: A48305; MUID:90254827; PMID:2340591
A:Accession: B48305
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-499 <KOR>
A:Cross-references: UNIPROT:Q02906
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:194-321/Domain: alpha-amylase core homology <AMY>

```

```

Query Match 100.0%; Score 7; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 SSQDYFH 7
DB 162 SSQDYFH 168

```

RESULT 9

JC4510
pullulanase (EC 3.2.1.41) precursor - yeast (*Lipomyces kononenkoae*)
N:Alternate names: LKAI protein; raw starch-degrading amylase
N:Contains: alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)
C:Species: *Lipomyces kononenkoae*
C>Date: 07-Feb-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
C:Accession: JC4510; PC4116
R:Steyn, A.J.C.; Marmur, J.; Pretorius, I.S.
Gene 166, 65-71, 1995
A:Title: Cloning, sequence analysis and expression in yeasts of a cDNA containing a lipoglucanase
A:Reference number: JC4510; MUID:96105202; PMID:8529895
A:Accession: JC4510
A:Molecule type: mRNA
A:Residues: 1-624 <STE>
A:Cross-references: UNIPROT:Q01117; GB:U03076; NID:g1173536; PIDN:AAC49622.1; PID:g1173536
A:Experimental source: strain IGC4052B
A:Accession: PC4116
A:Molecule type: protein
A:Residues: 29-44 <ST2>
A:Experimental source: IGC4052B
C:Genetics:
A:Gene: LKAI
C:Function:
A:Description: hydrolyzes raw starch, degrading both alpha-1,4 and alpha-1,6 linkages
A:Pathway: glycogen/starch degradation
C:Superfamily: *Lipomyces* alpha-amylase; alpha-amylase core homology; glucoamylase starch
C:Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-624/Product: alpha-amylase #status predicted <MAT>
F:48-141/Domain: glucoamylase starch-binding domain homology <SBD>
F:320-447/Domain: alpha-amylase core homology <AMY>
F:177-185,297-311,387-430,587-622/Dissulfide bonds: #status predicted
F:304,344/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:357,377,444/Active site: His, Glu, Asp #status predicted

Query Match 100.0%; Score 7; DB 1; Length 624;

Best Local Similarity 100.0%; Pred. No. 0.42;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7

Db 288 SSQDYFH 294

RESULT 10

E84088
restriction endonuclease (HaeIII) BH3509 [imported] - *Bacillus halodurans* (strain C-125)
C:Species: *Bacillus halodurans*
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: E84088
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A:Reference number: AB3650; MUID:20512582; PMID:11058132
A:Accession: E84088
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-317 <STO>
A:Cross-references: UNIPROT:Q9K764; GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BA8072
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3509

Query Match 85.7%; Score 6; DB 2; Length 317;

Best Local Similarity 100.0%; Pred. No. 3.6;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYF 6

Db 142 SSQDYF 147

RESULT 11

E86187
YUP8H12.10 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86187
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: AB6141; MUID:21016719; PMID:11130712
A:Accession: E86187
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-351 <STO>
A:Cross-references: UNIPROT:O23041; GB:AB005172; NID:g2388568; PIDN:AAB71449.1; GSPDB:G.
C:Genetics:
A:Map position: 1

Query Match 85.7%; Score 6; DB 2; Length 351;

Best Local Similarity 100.0%; Pred. No. 4;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYF 6

Db 226 SSQDYF 231

RESULT 12

S49803
hypothetical protein YML058w - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: hypothetical protein YM9958.04
C:Species: *Saccharomyces cerevisiae*
C>Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C:Accession: S49803
R:Devlin, K.; Churcher, C.
submitted to the EMBL Data Library, November 1994
A:Reference number: S49800
A:Accession: S49803
A:Molecule type: DNA
A:Residues: 1-104 <DEV>
A:Cross-references: UNIPROT:Q04964; EMBL:Z46729; NID:g577134; PIDN:CAA86717.1; PID:g57717.1
C:Genetics:
A:Gene: SGD:SM11; MIPS:YML058w
A:Cross-references: SGD:S0004523
A:Map position: 13L
C:Superfamily: *Saccharomyces* hypothetical protein YML058w

Query Match 71.4%; Score 5; DB 2; Length 104;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQDYF 6

Db 4 SQDYF 8

RESULT 13

H71046
hypothetical protein PH1664 - *Pyrococcus horikoshii*
C:Species: *Pyrococcus horikoshii*
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: H71046
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki,
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: H71046
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-129 <KAW>
A:Cross-references: UNIPROT:O59337; GB:AP000006; NID:G3236133; PIDN:BAA30776.1; PID:G325
A:Experimental source: strain OT3
A:Note: This accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1664

Query Match 71.4%; Score 5; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDY 5
|||||
DB 29 SSQDY 33

RESULT 14

JC7121
androgenic gland hormone precursor - common pill bug
C:Species: Armadillidium vulgare (common pill bug)
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: JC7121
R:Okuno, A.; Hasegawa, Y.; Ohira, T.; Katakura, Y.; Nagasawa, H.
Biochem. Biophys. Res. Commun. 264, 419-423, 1999
A:Title: Characterization and cDNA cloning of androgenic gland hormone of the terrestrial
A:Reference number: JC7121; MUID:20001935; PMID:10529379
A:Accession: JC7121
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-144 <OKU>
A:Cross-references: UNIPROT:Q9U8R2; DDBJ:AB029615; GB:AB029615; NID:G6446571; PID:G64465
A:Experimental source: androgenic gland

Query Match 71.4%; Score 5; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDYFH 7
|||||
DB 82 QDYFH 86

RESULT 15

H96905
hypothetical protein CAC0048 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: H96905
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: H96905
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-178 <KUR>
A:Cross-references: UNIPROT:Q97M21; GB:AE001437; PIDN:AAK78035.1; PID:G15022870; GSPDB:G
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0048

Query Match 71.4%; Score 5; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDY 5
|||||

Db 34 SSQDY 38

Search completed: November 7, 2005, 19:33:48
Job time : 1.85135 secs

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OM protein - protein search, using sw model

Run on: November 7, 2005, 19:00:20 ; Search time 3.71622 Seconds
(without alignments)
964.571 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167
Perfect score: 7
Sequence: 1 SSQDYFH 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 1612378 seqs, 512079187 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	7	100.0	498 1	AMYA ASPAW
2	7	100.0	498 2	Q76CT3
3	7	100.0	499 1	AMYA ASPOR
4	7	100.0	499 1	AMVB ASPAW
5	7	100.0	499 1	AMY APSH
6	7	100.0	499 2	Q96TH4
7	7	100.0	499 2	Q76LJ9
8	7	100.0	499 2	Q71LV45
9	7	100.0	624 1	AMV1_LIPKO
10	7	100.0	647 2	Q6VF33
11	6	85.7	183 2	Q8D239
12	6	85.7	183 2	Q8E4P7
13	6	85.7	261 2	Q73L56
14	6	85.7	295 2	Q6CUI2
15	6	85.7	317 2	Q9K764
16	6	85.7	351 2	Q23041
17	5	71.4	49	Q6XYZ7
18	5	71.4	72	Q6TQU2
19	5	71.4	87	Q76LJ94
20	5	71.4	97	Q8MZM1
21	5	71.4	98	Q677E1
22	5	71.4	104	SML1_YEAST
23	5	71.4	119	Q7VQH5
24	5	71.4	125	Q75IX1
25	5	71.4	129	Q59337
26	5	71.4	144	1 AGH ARMVU
27	5	71.4	163	Q9CUQ8
28	5	71.4	174	Q73QI6
29	5	71.4	177	Q7S6B6
30	5	71.4	178	Q97MZ1
31	5	71.4	180	Q97SK2

32	5	71.4	181	2	Q6IIG1	Q6iig1 drosophila
33	5	71.4	185	2	Q8E118	Q8e118 streptococc
34	5	71.4	199	1	TDX TRYBR	Q26695 trypanosoma
35	5	71.4	199	2	Q71RY2	Q71ry2 trypanosoma
36	5	71.4	199	2	Q71SQ4	Q71sq4 trypanosoma
37	5	71.4	205	2	Q9U4F2	Q9u4f2 hydra atten
38	5	71.4	215	2	P97975	P97975 unidentified
39	5	71.4	217	1	HMT2_YEAST	P49775 saccharomyc
40	5	71.4	218	2	Q9CUH8	Q9cuH8 mus musculu
41	5	71.4	222	2	Q6ZUU9	Q6zuu9 homo sapien
42	5	71.4	224	2	Q70BE3	Q70be3 pseudomonas
43	5	71.4	237	2	Q7M8C0	Q7m8c0 wolinnella s
44	5	71.4	248	2	Q7YSZ6	Q7ysz6 rhodnius pr
45	5	71.4	253	2	Q8EUT6	Q8eut6 mycoplasma

ALIGNMENTS

RESULT 1					
AMYA ASPAW					
ID	AMYA ASPAW	STANDARD;	PRT;	498 AA.	
AC	Q02905;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Alpha-amylase A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan				
DE	glucanohydrolase A).				
GN	Name=AMVA;				
OS	Aspergillus awamori.				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;				
OC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.				
OX	NCBI_TaxID=105351;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=UVK143F;				
RX	MEDLINE=90254827; PubMed-2340591;				
RA	Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,				
RA	Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;				
RT	"Cloning, characterization, and expression of two alpha-amylase genes				
RT	from Aspergillus niger var. awamori.";				
RL	Curr. Genet. 17:203-212(1990).				
CC	- - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic				
CC	linkages in oligosaccharides and polysaccharides.				
CC	- - COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory				
CC	at high concentrations (By similarity).				
CC	- - SIMILARITY: Belongs to the glycosyl hydrolase 13 family.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
CC	EMBL; X52755; CAA36966.1; --				
DR	PIR; A48305; A48305.				
DR	HSSP; P10529; 7TAA.				
DR	InterPro; IPR006589; Alp_amy1_cat_sub.				
DR	InterPro; IPR006047; Alpha_amy1_cat.				
DR	InterPro; IPR006046; Glyco_hydro_13.				
DR	Pfam; PF00128; Alpha-amylase; 1.				
DR	PRINTS; PR00110; ALPHAAMYLASE.				
DR	SMART; SM00642; Amy; 1.				
DR	Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;				
KW	Hydrolase; Multigene family; Signal.				
FT	SIGNAL 1 21 Potential.				
FT	CHAIN 22 498 Alpha-amylase A.				
FT	ACT_SITE 227 227 Nucleophile (By similarity).				
FT	ACT_SITE 251 251 Proton donor (By similarity).				
FT	ACT_SITE 318 318 By similarity.				
FT	METAL 142 142 Calcium 1 (By similarity).				

```

FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
FT METAL 196 196 similarity).
FT METAL 227 227 Calcium 1 (By similarity).
FT METAL 231 231 Calcium 2 (By similarity).
FT METAL 251 251 Calcium 1 (via carbonyl oxygen) (By
FT METAL 251 251 similarity).
FT DISULFID 51 59 Calcium 2 (By similarity).
FT DISULFID 171 185 By similarity.
FT DISULFID 261 304 By similarity.
FT DISULFID 461 496 By similarity.
FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 498 AA; 54880 MW; 7658511BC01A8A01 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 2
Q76CT3
ID Q76CT3 PRELIMINARY; PRT; 498 AA.
AC Q76CT3
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Alpha-amylase.
GN Name=amyA;
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RA Ito K.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB109452; BAD01051.1; -.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHA-AMYLASE.
DR SMART; SM00642; Aamy; 1.
SQ SEQUENCE 498 AA; 54679 MW; 8407BBFC7F4E3FC0 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 161 SSQDYFH 167

RESULT 3
AMYA_ASPOR
ID AMYA_ASPOR STANDARD; PRT; 499 AA.
AC P10529; P11763; Q00250;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase A precursor (EC 3.2.1.1) (Taka-amylase A) (TAA) (1,4-
DE alpha-D-glucan glucanohydrolase).
GN Name=AMY1;
GN and
GN Name=AMY2;

```

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GN and
GN Name=AMY3;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 63303;
RX MEDLINE=89237897; PubMed=2785629;
RA Wiersel S., Lachmund A., Wildhardt G., Rutkowski E.;
RT "Three alpha-amylase genes of Aspergillus oryzae exhibit identical
RT intron-exon organization.";
RL Mol. Microbiol. 3:3-14(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6;
RA Genes M.J., Dove M.J., Seligy V.L.;
RT "Aspergillus oryzae has two nearly identical Taka-amylase genes, each
RT containing eight introns.";
RL Gene 79:107-117(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Tada S., Iimura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.;
RT "Cloning and nucleotide sequence of the genomic Taka-amylase A gene of
RT Aspergillus oryzae.";
RL Agric. Biol. Chem. 53:593-599(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
RA Tsukagoshi N., Furukawa M., Nagaba H., Kirita N., Tsuboi A., Uda S.;
RT "Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A:
RT evidence for multiple related genes.";
RL Gene 84:319-327(1989).
RN [5]
RP SEQUENCE OF 22-499.
RA Toda H., Kondo K., Narita K.;
RT "The complete amino acid sequence of Taka-amylase A.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 58:208-212(1982).
RN [6]
RP SEQUENCE OF 206-225.
RX MEDLINE=74001521; PubMed=4733850;
RA Isemura S., Ikenaka T.;
RT "The amino acid sequences of glycopeptides obtained from Taka-amylase
RT A with trypsin and chymotrypsin.";
RL J. Biochem. 74:1-10(1973).
RN [7]
RP SEQUENCE OF 433-499.
RA Narita K.;
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=80227691; PubMed=6156152;
RA Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
RA Toda H., Narita K., Kakudo M.;
RT "Molecular structure of taka-amylase A. I. Backbone chain folding at
RT 3-A resolution.";
RL J. Biochem. 87:1555-1558(1980).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=84212370; PubMed=6609921;
RA Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
RT "Structure and possible catalytic residues of Taka-amylase A.";
RL J. Biochem. 95:697-702(1984).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
RX MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
RA Brzozowski A.M., Davies G.J.;
RT "Structure of the Aspergillus oryzae alpha-amylase complexed with the
RT inhibitor acarbose at 2.0-A resolution.";
RL Biochemistry 36:10837-10845(1997).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.

```

CC -|- COPACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations.
 CC -|- SUBUNIT: Monomer.
 CC -|- BIOTECHNOLOGY: Used in the brewing industry to increase the
 CC fermentability of beer worts (including those made from unmalted
 CC cereals), in the starch industry to make high maltose and high DE
 CC syrups (starch saccharification), in the alcohol industry to
 CC reduce fermentation time, in the cereal food industry for flour
 CC supplementation and improvement of chilled and frozen dough, and
 CC in the forestry industry for low-temperature modification of
 CC starch. Sold under the name Fungamyl by Novozymes.
 CC -|- MISCELLANEOUS: The sequence of AMV1 and AMY2 is shown.
 CC -|- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; X12725; CAA31218.1; -;
 CC DR EMBL; X12726; CAA31219.1; -;
 CC DR EMBL; X12727; CAA31220.1; -;
 CC DR EMBL; D00434; BAA00336.1; -;
 CC DR EMBL; M33218; AAA32708.1; -;
 CC DR PIR; JKO201; JKO201.
 CC DR PIR; JTO466; JTO466.
 CC DR PIR; S04548; ALAS1.
 CC DR PDB; 2TAA; X-ray; A=22-499.
 CC DR PDB; 6TAA; X-ray; @=22-499.
 CC DR PDB; 7TAA; X-ray; @=22-499.
 CC DR GlycoSuiteDB; P10529; -;
 CC DR InterPro; IPR006589; Alp_amy1_cat_sub.
 CC DR InterPro; IPR006047; Alpha_amy1_cat.
 CC DR InterPro; IPR006046; Glyco_hydro_13.
 CC DR Pfam; PF00128; Alpha-amy1ase; 1.
 CC DR PRINTS; PR00110; ALPHA-AMY1ASE.
 CC DR SMART; SM00642; Amy; 1.
 CC DR 3D-structure; Calcium-binding; Carbohydrate metabolism;
 CC Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
 CC Multigene family; Signal.
 CC SIGNAL 1 21
 CC CHAIN 22 499 Alpha-amy1ase A.
 CC ACT_SITE 227 227 Nucleophile.
 CC ACT_SITE 251 251 Proton donor.
 CC ACT_SITE 318 318
 CC METAL 142 142 Calcium 1.
 CC METAL 183 183 Calcium 1 (via carbonyl oxygen).
 CC METAL 196 196 Calcium 1.
 CC METAL 227 227 Calcium 2.
 CC METAL 231 231 Calcium 1 (via carbonyl oxygen).
 CC METAL 251 251 Calcium 2.
 CC DISULFID 51 59
 CC DISULFID 171 185
 CC DISULFID 261 304
 CC DISULFID 461 496
 CC CARBOHYD 218 218 N-linked (GlcNAc...)/
 CC VARIANT 56 56 /FTID=CAR_000125.
 CC VARIANT 172 172 Q -> R (in AMY3).
 CC CONFLICT 93 94 F -> L (in AMY3).
 CC CONFLICT 106 106 TT -> DC (in Ref. 5).
 CC CONFLICT 184 184 D -> T (in Ref. 5).
 CC CONFLICT 195 195 D -> Y (in Ref. 3).
 CC CONFLICT 195 195 P -> L (in Ref. 3).
 CC CONFLICT 255 255 D -> V (in Ref. 3).
 CC CONFLICT 291 291 D -> H (in Ref. 4).
 CC CONFLICT 345 345 I -> L (in Ref. 5).
 CC CONFLICT 370 370 L -> A (in Ref. 4).
 CC CONFLICT 406 409 WPY -> PY (in Ref. 5).
 CC CONFLICT 448 448 G -> S (in Ref. 5).
 CC CONFLICT 497 497 S -> SD (in Ref. 5 and 7).

FT HELIX 24 27
 FT TURN 28 29
 FT STRAND 32 35
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 FT STRAND 42 42
 FT TURN 43 44
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 FT STRAND 167 167
 FT TURN 176 177
 FT STRAND 179 184
 FT STRAND 186 188
 FT STRAND 192 194
 FT STRAND 196 197
 FT TURN 199 200
 FT HELIX 202 219
 FT TURN 220 220
 FT STRAND 223 226
 FT HELIX 229 231
 FT TURN 234 235
 FT HELIX 236 244
 FT TURN 245 245

Query Match 100.0%; Score 7; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 DB 162 SSQDYFH 168

RESULT 4
 AMYB_ASPAW
 ID AMYB_ASPAW STANDARD; PRT; 499 AA.
 AC Q02906;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alpha-amy1ase B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase B).
 GN Name=AMYB;
 OS Aspergillus awamori.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=105351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UVK143F;
 RX MEDLINE=90254827; PubMed=2340591;
 RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,

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RA Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
RT "Cloning, characterization, and expression of two alpha-amylase genes
RL from Aspergillus niger var. awamori.",
CC Curr. Genet. 17:203-212(1990).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X52756; CAA36967.1; -.
CC PIR; B48305; B48305.
CC HSP; F10529; 7TAA.
CC InterPro; IPR006589; Alp_amyl_cat_sub.
CC InterPro; IPR006047; Alpha_amyl_cat.
CC InterPro; IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; Alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAMYLASE.
CC SMART; SM00642; Amy; 1.
CC Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
KW Hydrolase; Multigene family; Signal.
FT SIGNAL 1 21
FT CHAIN 22 499
FT ACT_SITE 227 227
FT ACT_SITE 251 251
FT ACT_SITE 318 318
FT METAL 142 142
FT METAL 183 183
FT METAL 196 196
FT METAL 227 227
FT METAL 231 231
FT METAL 251 251
FT DISULFID 51 59
FT DISULFID 171 185
FT DISULFID 261 304
FT DISULFID 461 496
FT CARBOHYD 218 218
SQ SEQUENCE 499 AA; 54921 MW; 740B96B11BC01A8A CRC64;
Query Match 100.0%; Score 7; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.4; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;
QY 1 SSQDYFH 7
DB 162 SSQDYFH 168
RESULT 5
AMY ASPSH STANDARD; PRT; 499 AA.
AC P30292.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
DE Name=AMY;
OS Aspergillus shirousami.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5070;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=92323146; PubMed=1368777;
RA Shibuya I., Tamura G., Ishikawa T., Hara S.;
RT "Cloning of the alpha-amylase cDNA of Aspergillus shirousamii and its
RT expression in Saccharomyces cerevisiae.",
RL Biosci. Biotechnol. Biochem. 56:174-179(1992).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
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CC -----
CC EMBL; D10461; BAA01255.1; -.
CC HSP; F10529; 7TAA.
CC InterPro; IPR006589; Alp_amyl_cat_sub.
CC InterPro; IPR006047; Alpha_amyl_cat.
CC InterPro; IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; Alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAMYLASE.
CC SMART; SM00642; Amy; 1.
CC Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
KW Hydrolase; Signal.
FT SIGNAL 1 21
FT CHAIN 22 499
FT ACT_SITE 227 227
FT ACT_SITE 251 251
FT ACT_SITE 318 318
FT METAL 142 142
FT METAL 183 183
FT METAL 196 196
FT METAL 227 227
FT METAL 231 231
FT METAL 251 251
FT DISULFID 51 59
FT DISULFID 171 185
FT DISULFID 261 304
FT DISULFID 461 496
FT CARBOHYD 218 218
SQ SEQUENCE 499 AA; 54852 MW; 1FB7AE50DA01C03F CRC64;
Query Match 100.0%; Score 7; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.4; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;
QY 1 SSQDYFH 7
DB 162 SSQDYFH 168
RESULT 6
Q96TH4 PRELIMINARY; PRT; 499 AA.
AC Q96TH4.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Taka-amylase A (EC 3.2.1.1).
DE Name=amyA;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]

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Db 162 SSQDYFH 168

RESULT 8

Q7LV45	ID	Q7LV45	PRELIMINARY;	PRT;	499 AA.
AC	Q7LV45				
DT	05-JUL-2004	(TREMBLrel. 27, Created)			
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)			
DE	Alpha-amylase (EC 3.2.1.1).				
GN	Names-amyl;				
OS	Aspergillus flavus.				
OC	Eukaryota; Fungi; Ascomycota; Peizomycotina; Eurotiomycetes;				
OC	Euriales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.				
OX	NCBI_TaxID=5059;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=86-10D;				
RA	Fakhoury A.M., Woloshuk C.P.;				
RT	"Amyl, the alpha-amylase gene of Aspergillus flavus: Involvement in				
RT	afatoxin biosynthesis in maize kernels.";				
RL	Phytopathology 89:908-914(1999).				
CC	-1: SIMILARITY: Belongs to family 13 of glycosyl hydrolases.				
DR	ENBL; AF139925; AAF14264.1; -.				
GO	GO: 0004556; F:alpha-amylase activity; IEA.				
DR	GO: 0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.				
DR	GO: 0005975; P:carbohydrate metabolism; IEA.				
DR	InterPro: IPR006047; Alpha_amyl_cat.				
DR	InterPro: IPR006589; Alp_amyl_cat_sub.				
DR	InterPro: IPR006046; Glyco_hydro_13.				
DR	Pfam: PF00128; Alpha-amylase; 1.				
DR	PRINTS: PR00110; ALPHAAMYLASE.				
DR	SMART: SM00642; Amyv; 1.				
KW	Glycosidase; Hydrolase.				
SQ	SEQUENCE 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;				

Query Match 100.0%; Score 7; DB 2; Length 499;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 SSQDYFH 7
 |||||
 Db 162 SSQDYFH 168

RESULT 9

AMY1_LIPKO	ID	AMY1_LIPKO	STANDARD;	PRT;	624 AA.
AC	Q01117;				
DT	10-OCT-2003 (Rel. 42, Created)				
DT	10-OCT-2003 (Rel. 42, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan				
DE	glucanohydrolase 1).				
GN	Names=LKA1;				
OS	Lipomyces kononenkoae.				
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;				
OC	Saccharomycetales; Lipomycetaceae; Lipomyces.				
OX	NCBI_TaxID=34357;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=IGC4052B;				
EX	MEDLINE=96105202; PubMed=8529895; DOI=10.1016/0378-1119(95)00633-0;				
RT	Steyn A.J.C., Marmur J., Pretorius I.S.;				
RT	"Cloning, sequence analysis and expression in yeasts of a cDNA				
RL	containing a Lipomyces kononenkoae alpha-amylase-encoding gene.";				
RL	Gene 166:65-71(1995).				
RN	[2]				
RP	SEQUENCE OF 29-44.				
RC	STRAIN=IGC4052B;				
RX	MEDLINE=96132108; PubMed=8593683;				
RA	Steyn A.J.C., Pretorius I.S.;				

RT "Characterization of a novel alpha-amylase from *Lipomyces kononenkoae*
 RL and expression of its gene (LKAL1) in *Saccharomyces cerevisiae*.";
 CC Curr. Genet. 28:526-533 (1995).
 CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -|- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations (By similarity).
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC -|- SIMILARITY: Contains 1 carbohydrate binding type-21 (CBM21)
 CC domain.
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 CC
 CC EMBL; U30376; AAC49622.1; ALT_INIT.
 CC PIR; JC4510; JC4510.
 CC HSP; E10529; 7TAA.
 CC InterPro; IPR006589; Alp_aml_cat_sub.
 CC InterPro; IPR006047; Alpha_aml_cat.
 CC InterPro; IPR005036; CBM 21.
 CC Pfam; PF00128; Alpha-amylase; 1.
 CC Pfam; PF03370; CBM 21; 1.
 CC SMART; SM00642; Aamy; 1.
 CC Glycoprotein; Glycosidase; Hydrolase; Signal.
 KW Calcium-binding; Carbohydrate metabolism; Direct protein sequencing;
 KW Glycoprotein; Glycosidase; Hydrolase; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 624
 FT DOMAIN 40 133
 FT ACT_SITE 353 353
 FT ACT_SITE 377 377
 FT ACT_SITE 444 444
 FT METAL 268 268
 FT METAL 309 309
 FT METAL 322 322
 FT METAL 353 353
 FT METAL 357 357
 FT METAL 377 377
 FT DISULFID 177 185
 FT DISULFID 287 311
 FT DISULFID 387 430
 FT DISULFID 587 622
 FT CARBOHYD 304 304
 FT CARBOHYD 344 344
 SQ SEQUENCE 624 AA; 58876 MW; 87EB16534F5A9A9F CRC64;
 Query Match 100.0%; Score 7; DB 1; Length 624;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SSQDYFH 7
 DB 288 SSQDYFH 294
 RESULT 10
 Q6YF33 PRELIMINARY; PRT; 647 AA.
 AC Q6YF33;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Alpha-amylase.
 OS *Lipomyces starkeyi*.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Lipomycetaceae; Lipomyces.

OX NCBI_TaxID=29829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KSM 22W;
 RX PubMed=15043869; DOI=10.1016/j.femsle.2004.01.036;
 RA Kang H.K., Lee J.H., Kim D., Day D.F., Robyt J.F., Park K.-H.,
 Moon T.-W.;
 RT "Cloning and expression of *Lipomyces starkeyi* alpha-amylase in
 RT *Escherichia coli* and determination of some of its properties.";
 RL FEMS Microbiol. Lett. 233:53-64 (2004).
 DR EMBL; AY15463; AAN75021.1; -.
 DR HSSP; P26827; 1A47.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_aml_cat.
 DR InterPro; IPR006589; Alp_aml_cat_sub.
 DR InterPro; IPR005036; CBM 21.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR Pfam; PF03370; CBM 21; 1.
 DR SMART; SM00642; Aamy; 1.
 SQ SEQUENCE 647 AA; 70957 MW; D946071DB7560144 CRC64;
 Query Match 100.0%; Score 7; DB 2; Length 647;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SSQDYFH 7
 DB 311 SSQDYFH 317
 RESULT 11
 Q8DZ39 PRELIMINARY; PRT; 183 AA.
 AC Q8DZ39;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein SAG1281.
 GN OrderedLocustNames=SAG1281;
 OS *Streptococcus agalactiae* (serotype V).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC *Streptococcus*.
 OX NCBI_TaxID=216466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2603 V/R / Serotype V;
 RX MEDLINE=2222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
 RA Tettelin H., Massignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
 RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
 RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
 RA Radune D., Fedorova N.B., Scanlan D., Khouiri H.M., Mulligan S.,
 RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
 RA Iacobino E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
 RA Rancudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative genomic analysis of an
 RT emerging human pathogen, serotype V *Streptococcus agalactiae*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
 DR EMBL; AE014250; AAN00154.1; -.
 DR TIGR; SAG1281; -.
 KW Complete proteome.
 SQ SEQUENCE 183 AA; 21278 MW; 029AD020DF762720 CRC64;
 Query Match 85.7%; Score 6; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SSQDYFH 6
 DB 135 SSQDYFH 140

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RESULT 12
Q8E4P7
ID Q8E4P7 PRELIMINARY; PRT; 183 AA.
AC Q8E4P7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein gbs1354.
GN OrderedLocusNames=gbs1354;
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN [1]
RP SEQUENCE 183 AA; 21243 MW; 12A79C080C813D5C CRC64;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaser P., Rueniok C., Buchrieser C., Chevalier F., Frangeul L.,
RA Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease";
RL Mol. Microbiol. 45:1499-1513 (2002).
DR EMBL; AL766850; CAD47013.1; -.
DR Sagalish; gbs1354; -.
KW Complete proteome.
SQ SEQUENCE 183 AA; 21243 MW; 12A79C080C813D5C CRC64;

Query Match 85.7%; Score 6; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYF 6
Db 135 SSQDYF 140

RESULT 13
Q73L56
ID Q73L56 PRELIMINARY; PRT; 261 AA.
AC Q73L56;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TD2209;
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35405 / DSM 14222;
RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA Seshadri R., Myers G.S.A., Tettelin H., Bisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebregeorgis E., Geer K., Tshegaye G., Maick J.A., Ayodeji B.,
RA Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).
DR EMBL; AE017252; AA012523.1; -.
DR TIGR; TDE2009; -.
DR InterPro; IPR000504; RNA_rec_mot.
DR PROSITE; PS00030; RRM_RNF_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 261 AA; 30170 MW; 7F11DC42F0894499 CRC64;

Query Match 85.7%; Score 6; DB 2; Length 261;

Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYF 6
Db 123 SSQDYF 128

RESULT 14
Q6CUY2
ID Q6CUY2 PRELIMINARY; PRT; 295 AA.
AC Q6CUY2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Kluyveromyces lactis strain NRRL Y-1140 chromosome C of strain NRRL Y-
DE 1140 of Kluyveromyces lactis.
GN ORFNames=KLLA0C013869;
OS Kluyveromyces lactis NRRL Y-1140.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=284590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissiere A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382123; CAH01108.1; -.
DR GO; GO:0007163; P:signal transduction; IEA.
DR InterPro; IPR000159; RA.
DR InterPro; IPR010993; SAM_homology.
DR Pfam; PF00788; RA; 1.
DR SMART; SM00314; RA; 1.
DR PROSITE; PS50200; RA; 1.
SQ SEQUENCE 295 AA; 32546 MW; E6A28199F8830A06 CRC64;

Query Match 85.7%; Score 6; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYF 6
Db 138 SSQDYF 143

RESULT 15
Q9K764
ID Q9K764 PRELIMINARY; PRT; 317 AA.
AC Q9K764;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Restriction endonuclease (HaeIII).

```

GN OrderedLocusNames=BH3509;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirana C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001519; BAB07228.1; -.
DR PIR; E84088; E84088.
DR GO; GO:0004519; F:endonuclease activity; IEA.
KW Complete proteome; Endonuclease.
SQ SEQUENCE 317 AA; 36616 MW; 0860B7466391DC72 CRC64;

Query Match 85.7%; Score 6; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSQDYF 6
Db 142 SSQDYF 147

Search completed: November 7, 2005, 19:32:41
Job time : 5.71622 secs

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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:45:18 ; Search time 1.05405 Seconds
(without alignments)
495.746 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167

Perfect score: 7

Sequence: 1 SSQDYFH 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A-COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B-COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A-COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B-COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS-COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	478	1	US-08-720-899-7
2	7	100.0	478	1	US-08-459-610-7
3	7	100.0	478	2	US-08-343-804-7
4	7	100.0	478	2	US-08-339-715A-2
5	7	100.0	478	2	US-08-600-908A-10
6	7	100.0	478	3	US-08-683-838A-10
7	7	100.0	478	3	US-09-182-859-7
8	7	100.0	478	4	US-09-672-459-7
9	7	100.0	478	4	US-09-636-252A-10
10	7	100.0	478	4	US-10-186-042-7
11	5	71.4	84	4	US-09-583-110-4016
12	5	71.4	95	4	US-09-107-433-4442
13	5	71.4	113	4	US-09-248-796A-14523
14	5	71.4	153	4	US-09-369-247-166
15	5	71.4	153	4	US-09-270-767-47564
16	5	71.4	154	4	US-09-369-247-108
17	5	71.4	180	4	US-09-248-796A-22820
18	5	71.4	187	4	US-09-248-796A-19796
19	5	71.4	191	4	US-09-248-796A-22814
20	5	71.4	203	2	US-08-598-873-4
21	5	71.4	203	3	US-08-605-430-4
22	5	71.4	203	4	US-09-717-054-4
23	5	71.4	206	4	US-09-902-540-12425
24	5	71.4	210	4	US-09-248-796A-19369
25	5	71.4	303	4	US-09-328-352-5164
26	5	71.4	317	4	US-09-107-532A-4653
27	5	71.4	450	4	US-09-369-247-97

28	5	71.4	508	4	US-09-369-247-167	Sequence 167, Ap
29	5	71.4	550	1	US-08-143-219-25	Sequence 25, Appl
30	5	71.4	551	2	US-08-436-771-9	Sequence 9, Appli
31	5	71.4	551	2	US-08-434-998-9	Sequence 9, Appli
32	5	71.4	551	2	US-08-487-797-9	Sequence 9, Appli
33	5	71.4	551	4	US-09-949-016-6268	Sequence 6268, Ap
34	5	71.4	551	5	PCT-US95-02058-9	Sequence 9, Appli
35	5	71.4	577	4	US-09-248-796A-19304	Sequence 19304, A
36	5	71.4	590	4	US-09-248-796A-26874	Sequence 26874, A
37	5	71.4	591	4	US-09-949-016-11452	Sequence 11452, A
38	5	71.4	784	3	US-09-371-913A-7	Sequence 7, Appli
39	5	71.4	784	4	US-09-967-805-7	Sequence 7, Appli
40	5	71.4	788	4	US-09-107-532A-6538	Sequence 6538, Ap
41	5	71.4	792	4	US-09-134-000C-5895	Sequence 5895, Ap
42	5	71.4	974	4	US-09-252-991A-23640	Sequence 23640, A
43	5	71.4	998	4	US-09-252-991A-28424	Sequence 28424, A
44	5	71.4	1118	4	US-09-949-016-6596	Sequence 6596, Ap
45	5	71.4	1120	4	US-09-949-016-10404	Sequence 10404, A

ALIGNMENTS

RESULT 1

US-08-720-899-7
; Sequence 7, Application US/08720899
; Patent No. 5753460
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57534600 No. 5753460disk of No. 5753460ch America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,899
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-720-899-7

Query Match 100.0%; Score 7; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 SSQDYFH 7
Db      141 SSQDYFH 147

RESULT 2
US-08-459-610-7
; Sequence 7, Application US/08459610
; Patent No. 5801043
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 5801043o No. 5801043disk of No. 5801043th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,610
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-459-610-7

Query Match      100.0%; Score 7; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSQDYFH 7
Db      141 SSQDYFH 147

RESULT 3
US-08-343-804-7
; Sequence 7, Application US/08343804
; Patent No. 5830837
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 5830837o No. 5830837disk of No. 5830837th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,804
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-459-610-7

Query Match      100.0%; Score 7; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSQDYFH 7
Db      141 SSQDYFH 147

RESULT 4
US-08-339-715A-2
; Sequence 2, Application US/08339715A
; Patent No. 5965442
; GENERAL INFORMATION:
; APPLICANT: Kaneko, Hiroki
; APPLICANT: Takada, Toshikazu
; APPLICANT: Shimada, Jiro
; APPLICANT: Kuriaki, Takashi
; APPLICANT: Yanase, Michiyo
; APPLICANT: Takata, Hiroki
; APPLICANT: Okada, Shigetaka
; TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESS: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
; STREET: Metropolitan Square Building, Suite 800, 1450
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,715A
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: JP 306096/1993
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; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiser, Allen S.
; REGISTRATION NUMBER: 27,215
; REFERENCE/DOCKET NUMBER: 18335.009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-824-8000
; TELEFAX: 202-824-8199
; TELEX: 248516
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-339-715A-2

Query Match 100.0%; Score 7; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 5
US-08-600-908A-10
; Sequence 10, Application US/08600908A
; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: '-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5989169o No. 5989169disk of No. 5989169th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-600-908A-10

Query Match 100.0%; Score 7; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 6
US-08-683-838A-10
; Sequence 10, Application US/08683838A
; Patent No. 6022724
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: '-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6022724o No. 6022724disk of No. 6022724th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-683-838A-10

Query Match 100.0%; Score 7; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 7
US-09-182-859-7
; Sequence 7, Application US/09182859
; Patent No. 6143708
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisg rd-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/182,859
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: 0515/96
; EARLIER FILING DATE: 1996-04-30
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; EARLIER APPLICATION NUMBER: 0712/96
; EARLIER FILING DATE: 1996-06-28
; EARLIER APPLICATION NUMBER: 0775/96
; EARLIER FILING DATE: 1996-07-11
; EARLIER APPLICATION NUMBER: 1263/96
; EARLIER FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-182-859-7
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Query Match 100.0%; Score 7; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SSQDYFH 7
DB 141 SSQDYFH 147
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RESULT 8
US-09-672-459-7
; Sequence 7, Application US/09672459
; Patent No. 6436888
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-672-459-7
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Query Match 100.0%; Score 7; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SSQDYFH 7
DB 141 SSQDYFH 147
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RESULT 9
US-09-636-252A-10
; Sequence 10, Application US/09636252A
; Patent No. 6440716
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/09/636,252A
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; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-09-636-252A-10
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Query Match 100.0%; Score 7; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SSQDYFH 7
DB 141 SSQDYFH 147
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RESULT 10
US-10-186-042-7
; Sequence 7, Application US/10186042
; Patent No. 6642044
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7
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Query Match 100.0%; Score 7; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SSQDYFH 7
DB 141 SSQDYFH 147
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RESULT 11
US-09-583-110-4016
; Sequence 4016, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
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; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4016
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4016

Query Match 71.4%; Score 5; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDYFH 7
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Db 40 QDYFH 44

RESULT 12
US-107-433-4442
; Sequence 4442, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4442:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:

NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...95
SEQUENCE DESCRIPTION: SEQ ID NO: 4442:
US-09-107-433-4442

Query Match 71.4%; Score 5; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDYFH 7
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Db 51 QDYFH 55

RESULT 13
US-09-248-796A-14523
; Sequence 14523, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14523
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14523

Query Match 71.4%; Score 5; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQDYF 6
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Db 43 SQDYF 47

RESULT 14
US-09-369-247-166
; Sequence 166, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024PI
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 166
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-369-247-166

Query Match 71.4%; Score 5; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQDYF 6

Db 124 SQDYF 128

RESULT 15
US-09-270-767-47564
; Sequence 47564, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47564
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-47564

Query Match 71.4%; Score 5; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQDYF 6
Db 1 SQDYP 5

Search completed: November 7, 2005, 19:00:10
Job time : 2.05405 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:58:04 ; Search time 3.74324 Seconds
(without alignments)
782.441 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167

Perfect score: 7

Sequence: 1 SSQDYFH 7

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Gapop 60.0 , Gapext 60.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	7	100.0	476	17	US-10-877-849-43
2	7	100.0	478	14	US-10-184-771-10
3	7	100.0	478	14	US-10-186-042-7
4	7	100.0	478	15	US-10-644-187-7
5	7	100.0	478	17	US-10-926-720-10
6	7	100.0	478	17	US-10-980-759-7
7	7	100.0	478	20	US-11-064-196-10
8	7	100.0	498	16	US-10-815-495-22
9	7	100.0	498	16	US-10-820-200-2
10	7	100.0	498	17	US-10-877-849-30
11	7	100.0	499	16	US-10-815-495-18

12	7	100.0	499	16	US-10-797-393A-5	Sequence 5, Appli
13	7	100.0	608	17	US-10-877-849-40	Sequence 40, Appl
14	7	100.0	640	17	US-10-877-849-36	Sequence 36, Appl
15	7	100.0	1095	14	US-10-228-063-45	Sequence 45, Appl
16	5	71.4	55	16	US-10-425-115-307711	Sequence 307711,
17	5	71.4	59	16	US-10-425-115-325770	Sequence 325770,
18	5	71.4	60	15	US-10-424-599-212201	Sequence 212201,
19	5	71.4	61	15	US-10-424-599-153435	Sequence 153435,
20	5	71.4	65	16	US-10-423-115-281545	Sequence 281545,
21	5	71.4	73	16	US-10-437-963-182457	Sequence 182457,
22	5	71.4	82	15	US-10-424-599-162468	Sequence 162468,
23	5	71.4	82	15	US-10-424-599-164927	Sequence 164927,
24	5	71.4	82	16	US-10-437-963-113292	Sequence 113292,
25	5	71.4	86	16	US-10-425-115-355307	Sequence 355307,
26	5	71.4	89	16	US-10-425-115-287848	Sequence 287848,
27	5	71.4	92	15	US-10-424-599-226734	Sequence 226734,
28	5	71.4	94	20	US-11-097-143-41466	Sequence 41466, A
29	5	71.4	95	18	US-10-617-320-4442	Sequence 4442, Ap
30	5	71.4	104	9	US-09-814-661A-2	Sequence 2, Appli
31	5	71.4	110	16	US-10-437-963-123791	Sequence 123791,
32	5	71.4	116	16	US-10-767-701-33822	Sequence 33822, A
33	5	71.4	119	15	US-10-424-599-155789	Sequence 155789,
34	5	71.4	126	16	US-10-425-115-319361	Sequence 319361,
35	5	71.4	134	18	US-10-773-236-387	Sequence 387, App
36	5	71.4	152	16	US-10-425-115-271310	Sequence 271310,
37	5	71.4	153	14	US-10-082-548-166	Sequence 166, App
38	5	71.4	153	17	US-10-918-446-166	Sequence 166, App
39	5	71.4	153	19	US-11-002-755-166	Sequence 166, App
40	5	71.4	153	20	US-11-002-756-166	Sequence 166, App
41	5	71.4	154	14	US-10-062-548-108	Sequence 108, App
42	5	71.4	154	17	US-10-918-446-108	Sequence 108, App
43	5	71.4	154	19	US-11-002-755-108	Sequence 108, App
44	5	71.4	154	20	US-11-002-756-108	Sequence 108, App
45	5	71.4	171	15	US-10-424-599-169013	Sequence 169013,

ALIGNMENTS

RESULT 1
US-10-877-849-43
; Sequence 43, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)..(476)
US-10-877-849-43

Query Match 100.0%; Score 7; DB 17; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.7; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

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RESULT 2
US-10-184-771-10
; Sequence 10, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1f216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-10-184-771-10

Query Match          100.0%; Score 7; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 141 SSQDYFH 147

RESULT 3
US-10-186-042-7
; Sequence 7, Application US/10186042
; Publication No. US20030171236A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match          100.0%; Score 7; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 141 SSQDYFH 147

RESULT 4
US-10-644-187-7
; Sequence 7, Application US/10644187
; Publication No. US20040048351A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/644,187
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-644-187-7

Query Match          100.0%; Score 7; DB 15; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 141 SSQDYFH 147

RESULT 5
US-10-926-720-10
; Sequence 10, Application US/10926720
; Publication No. US20050019886A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/926,720
; FILING DATE: 26-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIORITY INFORMATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
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; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10

Query Match 100.0%; Score 7; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 6

US-10-980-759-7
; Sequence 7, Application US/10980759
; Publication No. US20050118695A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/980,759
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-980-759-7

Query Match 100.0%; Score 7; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 7

US-11-064-196-10
; Sequence 10, Application US/11064196
; Publication No. US20050170487A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants

; FILE REFERENCE: 0776/11216-US2
; CURRENT APPLICATION NUMBER: US/11/064,196
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-11-064-196-10

Query Match 100.0%; Score 7; DB 20; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 8

US-10-815-495-22
; Sequence 22, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connelly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; TITLE OF INVENTION: Mutants Of Aspergillus Niger
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-22

Query Match 100.0%; Score 7; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 9

US-10-820-200-2
; Sequence 2, Application US/10820200
; Publication No. US20040229764A1
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Pedersen, Sven
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
; FILE REFERENCE: 5835.200-US
; CURRENT APPLICATION NUMBER: US/10/820,200
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US/09/710,339
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/165,786
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2

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; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus Oryzae
US-10-820-200-2

Query Match      100.0%; Score 7; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 161 SSQDYFH 167

RESULT 10
US-10-877-849-30
; Sequence 30, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-877-849-30

Query Match      100.0%; Score 7; DB 17; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 161 SSQDYFH 167

RESULT 11
US-10-815-495-18
; Sequence 18, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connolly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; TITLE OF INVENTION: Mutants Of Aspergillus Niger
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-18

Query Match      100.0%; Score 7; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 161 SSQDYFH 167
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Db 162 SSQDYFH 168

RESULT 12
US-10-797-393A-5
; Sequence 5, Application US/10797393A
; Publication No. US20040219649A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Hans Sejr
; APPLICANT: Pedersen, Sven
; APPLICANT: Festeren, Rikke Monica
; TITLE OF INVENTION: ALCOHOL PRODUCT PROCESSES
; FILE REFERENCE: 10391.200-US
; CURRENT APPLICATION NUMBER: US/10/797,393A
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-797-393A-5

Query Match      100.0%; Score 7; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 13
US-10-877-849-40
; Sequence 40, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-40

Query Match      100.0%; Score 7; DB 17; Length 608;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 161 SSQDYFH 167

RESULT 14
US-10-877-849-36
; Sequence 36, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
```

; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-36

Query Match 100.0%; Score 7; DB 17; Length 640;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 161 SSQDYFH 167

RESULT 15
US-10-228-063-45
; Sequence 45, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lananan, Mike
; TITLE OF INVENTION: Self-processing Plants and Plant Parts
; FILE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Aspergillus shirousami
US-10-228-063-45

Query Match 100.0%; Score 7; DB 14; Length 1095;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

Search completed: November 7, 2005, 19:22:50
Job time : 3.74324 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:58:04 ; Search time 266.305 Seconds
(without alignments)
782.441 Million cell updates/sec

Title: US-10-820-200-2
Perfect score: 498
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Gapop 60.0 , Gapext 60.0

Searched: 1867879 seqs, 418409474 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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 - 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	498	100.0	498	17	US-10-877-849-30
3	498	100.0	499	16	US-10-797-393A-5
4	498	100.0	508	17	US-10-877-849-40
5	498	100.0	640	17	US-10-877-849-36
6	476	95.6	476	17	US-10-877-849-43
7	391	78.5	478	14	US-10-184-771-10
8	391	78.5	478	14	US-10-186-042-7
9	391	78.5	478	15	US-10-644-187-7
10	391	78.5	478	17	US-10-926-720-10
11	391	78.5	478	17	US-10-980-759-7

12	391	78.5	478	20	US-11-064-196-10	Sequence 10, Appl
13	384	77.1	498	16	US-10-815-495-22	Sequence 22, Appl
14	384	77.1	499	16	US-10-815-495-18	Sequence 18, Appl
15	377	75.7	1095	14	US-10-228-063-45	Sequence 45, Appl
16	23	4.6	495	14	US-10-213-990-42	Sequence 42, Appl
17	20	4.0	494	17	US-10-486-868-13	Sequence 13, Appl
18	19	3.8	513	15	US-10-369-493-2223	Sequence 2223, Ap
19	18	3.6	630	14	US-10-213-990-45	Sequence 45, Appl
20	14	2.8	505	17	US-10-877-849-42	Sequence 42, Appl
21	14	2.8	511	17	US-10-877-849-8	Sequence 8, Appl
22	14	2.8	609	17	US-10-877-849-38	Sequence 38, Appl
23	14	2.8	629	17	US-10-877-849-34	Sequence 34, Appl
24	14	2.8	640	17	US-10-877-007-22	Sequence 22, Appl
25	14	2.8	640	17	US-10-877-849-32	Sequence 32, Appl
26	14	2.8	640	17	US-10-877-849-41	Sequence 41, Appl
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28	12	2.4	500	15	US-10-369-493-12469	Sequence 12469, A
29	12	2.4	547	14	US-10-213-990-48	Sequence 48, Appl
30	12	2.4	549	17	US-10-486-868-14	Sequence 14, Appl
31	12	2.4	555	17	US-10-486-868-15	Sequence 15, Appl
32	11	2.2	484	15	US-10-416-393-1	Sequence 1, Appl
33	11	2.2	484	16	US-10-797-393A-1	Sequence 1, Appl
34	10	2.0	263	16	US-10-425-115-291647	Sequence 291647,
35	9	1.8	90	16	US-10-437-963-169831	Sequence 169831,
36	9	1.8	421	14	US-10-156-761-13129	Sequence 13129, A
37	9	1.8	561	15	US-10-369-493-12810	Sequence 12810, A
38	8	1.6	58	16	US-10-767-701-50236	Sequence 50236, A
39	8	1.6	84	15	US-10-424-599-284520	Sequence 284520,
40	8	1.6	105	16	US-10-437-963-125916	Sequence 125916,
41	8	1.6	134	16	US-10-437-963-129535	Sequence 129535,
42	8	1.6	258	16	US-10-432-934-78	Sequence 78, Appl
43	8	1.6	400	15	US-10-282-122A-50565	Sequence 50565, A
44	8	1.6	454	16	US-10-437-963-143998	Sequence 143998,
45	8	1.6	494	20	US-11-097-143-26370	Sequence 26370, A

ALIGNMENTS

RESULT 1
US-10-820-200-2
; Sequence 2, Application US/10820200
; Publication No. US20040229764A1
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Pedersen, Sven
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
; FILE REFERENCE: 5835:200-US
; CURRENT APPLICATION NUMBER: US/10/820,200
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US/09/710,339
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/165,786
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus Oryzae
US-10-820-200-2

Query Match	100.0%	Score 498;	DB 16;	Length 498;
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Db 61 TWQGIIDKLDYIQGMGFTAIWITPVTQALPQTAYGDAYHGYWQDIYSLNENYGTADDL 120
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Db 121 KALSSALHERGMYLWVDVVAHMGVDGAGSSVDYSVFKPFSSQDYFHFPCFIQNYEDQTQ 180
Qy 181 VEDCWLGNVTSLPDLDTTKDVKWNEWYDWVGLSVNSYSDGLRDTTKVHKQKDFWPGYN 240
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Db 241 KAAGYVCIGEVLDGDPAYTCYQNVMDGVLNPIIYPLLNAPKSTSGSMDDLYNNINTVK 300
Qy 301 SDPCDSTLLGTFVENHNDNPRFASYNDAIANKVAFAFIILNDGIPIIYAGQEHYAGGND 360
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Qy 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 420
Db 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 420
Qy 421 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTGVSDGNVVPVMAGGLP 480
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Qy 481 RVLYPTEKLAGSKICSSS 498
Db 481 RVLYPTEKLAGSKICSSS 498

RESULT 2

US-10-877-849-30
; Sequence 30, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikeo-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-877-849-30

Query Match 100.0%; Score 498; DB 17; Length 498;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 TWQGIIDKLDYIQGMGFTAIWITPVTQALPQTAYGDAYHGYWQDIYSLNENYGTADDL 120
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Qy 181 VEDCWLGNVTSLPDLDTTKDVKWNEWYDWVGLSVNSYSDGLRDTTKVHKQKDFWPGYN 240
Db 181 VEDCWLGNVTSLPDLDTTKDVKWNEWYDWVGLSVNSYSDGLRDTTKVHKQKDFWPGYN 240

Qy 241 KAAGYVCIGEVLDGDPAYTCYQNVMDGVLNPIIYPLLNAPKSTSGSMDDLYNNINTVK 300
Db 241 KAAGYVCIGEVLDGDPAYTCYQNVMDGVLNPIIYPLLNAPKSTSGSMDDLYNNINTVK 300
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Qy 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 420
Db 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 420
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Db 421 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTGVSDGNVVPVMAGGLP 480
Qy 481 RVLYPTEKLAGSKICSSS 498
Db 481 RVLYPTEKLAGSKICSSS 498

RESULT 3

US-10-797-393A-5
; Sequence 5, Application US/10797393A
; Publication No. US20040219649A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Hans Sejr
; APPLICANT: Pedersen, Sven
; APPLICANT: Festeren, Rikke Monica
; TITLE OF INVENTION: ALCOHOL PRODUCT PROCESSES
; FILE REFERENCE: 10391.200-US
; CURRENT APPLICATION NUMBER: US/10/797,393A
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-797-393A-5

Query Match 100.0%; Score 498; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 TWQGIIDKLDYIQGMGFTAIWITPVTQALPQTAYGDAYHGYWQDIYSLNENYGTADDL 120
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Qy 241 KAAGYVCIGEVLDGDPAYTCYQNVMDGVLNPIIYPLLNAPKSTSGSMDDLYNNINTVK 300
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QY 481 RVLYPEKLAGSKICSSS 498
Db 482 RVLYPEKLAGSKICSSS 499

RESULT 4
US-10-877-849-40
; Sequence 40, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-40

Query Match 100.0%; Score 498; DB 17; Length 608;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGGTTCNTADQKCGG 60
Db 1 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGGTTCNTADQKCGG 60
QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL 120
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Db 121 KALSALHERGMYLMDVVVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQIQ 180
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Db 301 SDPCPSTLLGTFVFNHNDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGQSHYAGND 360
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Db 361 PANREATWLSGYPTDSELYKLASANAIRNVAISKDTGFVTKNMPYIKDDTTIAMRKT 420
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Db 421 DGSQIVTILSNKGASDSTYLSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPPVPMAGGLP 480
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Db 482 RVLYPEKLAGSKICSSS 499

Db 481 RVLYPEKLAGSKICSSS 498

RESULT 5
US-10-877-849-36
; Sequence 36, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-36

Query Match 100.0%; Score 498; DB 17; Length 640;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGGTTCNTADQKCGG 60
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QY 181 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240
Db 181 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240
QY 241 KAAGYVCIGEVLDGDPAYTCPYQNVMDGVLYNPIYYPPLNAPKSTSGSMDDLYNNINTVK 300
Db 241 KAAGYVCIGEVLDGDPAYTCPYQNVMDGVLYNPIYYPPLNAPKSTSGSMDDLYNNINTVK 300
QY 301 SDPCPSTLLGTFVFNHNDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGQSHYAGND 360
Db 301 SDPCPSTLLGTFVFNHNDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGQSHYAGND 360
QY 361 PANREATWLSGYPTDSELYKLASANAIRNVAISKDTGFVTKNMPYIKDDTTIAMRKT 420
Db 361 PANREATWLSGYPTDSELYKLASANAIRNVAISKDTGFVTKNMPYIKDDTTIAMRKT 420
QY 421 DGSQIVTILSNKGASDSTYLSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPPVPMAGGLP 480
Db 421 DGSQIVTILSNKGASDSTYLSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPPVPMAGGLP 480
QY 481 RVLYPEKLAGSKICSSS 498
Db 481 RVLYPEKLAGSKICSSS 498

RESULT 6
US-10-877-849-43
; Sequence 43, Application US/10877849
; Publication No. US20050054071A1

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; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Takagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikeo-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 43
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
; NAME/KEY: mat_peptide
; LOCATION: (1)..(476)
US-10-877-849-43

Query Match      95.6%; Score 476; DB 17; Length 476;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      21 ATPADWRSQSIYFLLTDRPARTDGSSTTATCNTADOKYCGGTWQGIIDKLDYIQGMGFTAI 80
Db      1 ATPADWRSQSIYFLLTDRPARTDGSSTTATCNTADOKYCGGTWQGIIDKLDYIQGMGFTAI 60

Qy      81 WITPVTQALPQTAYGDAYHGYYWQDIYSLNENYGTADDLKSALSSALHERGMVLDVVA 140
Db      61 WITPVTQALPQTAYGDAYHGYYWQDIYSLNENYGTADDLKSALSSALHERGMVLDVVA 120

Qy      141 NHMGYDAGSSVDYVFPKPFSSQDYFHPFCFQNYEDQTVEDCWLGDNVTSPLDITTK 200
Db      121 NHMGYDAGSSVDYVFPKPFSSQDYFHPFCFQNYEDQTVEDCWLGDNVTSPLDITTK 180

Qy      201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYCI GEVLDDGDPAYTC 260
Db      191 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYCI GEVLDDGDPAYTC 240

Qy      261 PYQNVMDGVLYPIYPLLNAFKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDNR 320
Db      241 PYQNVMDGVLYPIYPLLNAFKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDNR 300

Qy      321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEOHYAGGNDPANREATWLSGYPTDSELYK 380
Db      301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEOHYAGGNDPANREATWLSGYPTDSELYK 360

Qy      381 LIASANAIRNVAISKDTGFVTKNWPYKDDTIAMRKGTGDSQIVTILSKNGASGDSYT 440
Db      361 LIASANAIRNVAISKDTGFVTKNWPYKDDTIAMRKGTGDSQIVTILSKNGASGDSYT 420

Qy      441 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICS 496
Db      421 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICS 476

RESULT 7
US-10-184-771-10
; Sequence 10, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/IF216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
;
```

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; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-10-184-771-10

Query Match      78.5%; Score 391; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      21 ATPADWRSQSIYFLLTDRPARTDGSSTTATCNTADOKYCGGTWQGIIDKLDYIQGMGFTAI 80
Db      1 ATPADWRSQSIYFLLTDRPARTDGSSTTATCNTADOKYCGGTWQGIIDKLDYIQGMGFTAI 60

Qy      81 WITPVTQALPQTAYGDAYHGYYWQDIYSLNENYGTADDLKSALSSALHERGMVLDVVA 140
Db      61 WITPVTQALPQTAYGDAYHGYYWQDIYSLNENYGTADDLKSALSSALHERGMVLDVVA 120

Qy      141 NHMGYDAGSSVDYVFPKPFSSQDYFHPFCFQNYEDQTVEDCWLGDNVTSPLDITTK 200
Db      121 NHMGYDAGSSVDYVFPKPFSSQDYFHPFCFQNYEDQTVEDCWLGDNVTSPLDITTK 180

Qy      201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYCI GEVLDDGDPAYTC 260
Db      191 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYCI GEVLDDGDPAYTC 240

Qy      261 PYQNVMDGVLYPIYPLLNAFKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDNR 320
Db      241 PYQNVMDGVLYPIYPLLNAFKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDNR 300

Qy      321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEOHYAGGNDPANREATWLSGYPTDSELYK 380
Db      301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEOHYAGGNDPANREATWLSGYPTDSELYK 360

Qy      381 LIASANAIRNVAISKDTGFVTKNWPYKDD 411
Db      361 LIASANAIRNVAISKDTGFVTKNWPYKDD 391

RESULT 8
US-10-186-042-7
; Sequence 7, Application US/10186042
; Publication No. US20030171236A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
;
```

US-10-186-042-7

Query Match 78.5%; Score 391; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
DB 1 ATPADWRSQSIYFLLTDRFARTDGTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60

QY 81 WITPVTALPQTAYGDAYHYGWQDIYSLNENYGTADDL KALSSALHERGMVLDVVA 140
DB 61 WITPVTALPQTAYGDAYHYGWQDIYSLNENYGTADDL KALSSALHERGMVLDVVA 120

QY 141 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFQNYEDQTVEDCWLGDNVTSLPDLDTTK 200
DB 121 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFQNYEDQTVEDCWLGDNVTSLPDLDTTK 180

QY 201 DVVKNWYDVGSLVSNYSIDGLRIDTVKHVKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
DB 181 DVVKNWYDVGSLVSNYSIDGLRIDTVKHVKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240

QY 261 PYQNVMDGVLNPIIYPLNNAFKSTSGMDDLNNMINTVKS DCPDSTLLGTFFVENHDNPR 320
DB 241 PYQNVMDGVLNPIIYPLNNAFKSTSGMDDLNNMINTVKS DCPDSTLLGTFFVENHDNPR 300

QY 321 FASYTNDIALAKNVAFIILNDGIPIIYAGQHQH YAGNDPANREATWLSGYPTDSELYK 380
DB 301 FASYTNDIALAKNVAFIILNDGIPIIYAGQHQH YAGNDPANREATWLSGYPTDSELYK 360

QY 381 LIASANAIRNYAISKDTGFVTKNWPYIKDD 411
DB 361 LIASANAIRNYAISKDTGFVTKNWPYIKDD 391

RESULT 9

US-10-644-187-7
; Sequence 7, Application US/10644187
; Publication No. US2004048351A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/644,187
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-644-187-7

Query Match 78.5%; Score 391; DB 15; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
DB 1 ATPADWRSQSIYFLLTDRFARTDGTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60

QY 81 WITPVTALPQTAYGDAYHYGWQDIYSLNENYGTADDL KALSSALHERGMVLDVVA 140
DB 61 WITPVTALPQTAYGDAYHYGWQDIYSLNENYGTADDL KALSSALHERGMVLDVVA 120

QY 141 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFQNYEDQTVEDCWLGDNVTSLPDLDTTK 200
DB 121 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFQNYEDQTVEDCWLGDNVTSLPDLDTTK 180

QY 201 DVVKNWYDVGSLVSNYSIDGLRIDTVKHVKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
DB 181 DVVKNWYDVGSLVSNYSIDGLRIDTVKHVKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240

QY 261 PYQNVMDGVLNPIIYPLNNAFKSTSGMDDLNNMINTVKS DCPDSTLLGTFFVENHDNPR 320
DB 241 PYQNVMDGVLNPIIYPLNNAFKSTSGMDDLNNMINTVKS DCPDSTLLGTFFVENHDNPR 300

QY 321 FASYTNDIALAKNVAFIILNDGIPIIYAGQHQH YAGNDPANREATWLSGYPTDSELYK 380
DB 301 FASYTNDIALAKNVAFIILNDGIPIIYAGQHQH YAGNDPANREATWLSGYPTDSELYK 360

QY 381 LIASANAIRNYAISKDTGFVTKNWPYIKDD 411
DB 361 LIASANAIRNYAISKDTGFVTKNWPYIKDD 391

RESULT 10

US-10-926-720-10
; Sequence 10, Application US/10926720
; Publication No. US20050019886A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/926,720
; FILING DATE: 26-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10

Query Match 78.5%; Score 391; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNADOKYCGGTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNADOKYCGGTWQGIIDKLDYIQGMGFTAI 60

QY 81 WITPVTAQLPQTAYGDAYHGYWQODIYSLNENYGTADDLKALSALHERGMVMDVVA 140
Db 61 WITPVTAQLPQTAYGDAYHGYWQODIYSLNENYGTADDLKALSALHERGMVMDVVA 120

QY 141 NHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNTVSLPDLDTTK 200
Db 121 NHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNTVSLPDLDTTK 180

QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYCI GEVLDDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYCI GEVLDDGDPAYTC 240

QY 261 PYQNVMDGVNLNPIYIYPLNNAFKSTSGMDDLNNMINTVKSDCPDSTLLGTFFVENHDNPR 320
Db 241 PYQNVMDGVNLNPIYIYPLNNAFKSTSGMDDLNNMINTVKSDCPDSTLLGTFFVENHDNPR 300

QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSLYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSLYK 360

QY 381 LIASANAIRNVAISKDTGFVTYKNWPIYKDD 411
Db 361 LIASANAIRNVAISKDTGFVTYKNWPIYKDD 391

RESULT 11

US-10-980-759-7
; Sequence 7, Application US/10980759
; Publication No. US20050118695A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796-204-US
; CURRENT APPLICATION NUMBER: US/10/980,759
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis

Query Match 78.5%; Score 391; DB 17; Length 478;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNADOKYCGGTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNADOKYCGGTWQGIIDKLDYIQGMGFTAI 60

QY 81 WITPVTAQLPQTAYGDAYHGYWQODIYSLNENYGTADDLKALSALHERGMVMDVVA 140

Db 61 WITPVTAQLPQTAYGDAYHGYWQODIYSLNENYGTADDLKALSALHERGMVMDVVA 120

QY 141 NHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNTVSLPDLDTTK 200
Db 121 NHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNTVSLPDLDTTK 180

QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYCI GEVLDDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYCI GEVLDDGDPAYTC 240

QY 261 PYQNVMDGVNLNPIYIYPLNNAFKSTSGMDDLNNMINTVKSDCPDSTLLGTFFVENHDNPR 320
Db 241 PYQNVMDGVNLNPIYIYPLNNAFKSTSGMDDLNNMINTVKSDCPDSTLLGTFFVENHDNPR 300

QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSLYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSLYK 360

QY 381 LIASANAIRNVAISKDTGFVTYKNWPIYKDD 411
Db 361 LIASANAIRNVAISKDTGFVTYKNWPIYKDD 391

RESULT 12

US-11-064-196-10
; Sequence 10, Application US/11064196
; Publication No. US20050170487A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/11/064,196
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae

Query Match 78.5%; Score 391; DB 20; Length 478;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNADOKYCGGTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNADOKYCGGTWQGIIDKLDYIQGMGFTAI 60

QY 81 WITPVTAQLPQTAYGDAYHGYWQODIYSLNENYGTADDLKALSALHERGMVMDVVA 140
Db 61 WITPVTAQLPQTAYGDAYHGYWQODIYSLNENYGTADDLKALSALHERGMVMDVVA 120

QY 141 NHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNTVSLPDLDTTK 200
Db 121 NHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNTVSLPDLDTTK 180

QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYCI GEVLDDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYCI GEVLDDGDPAYTC 240

QY 261 PYQNVMDGVNLNPIYIYPLNNAFKSTSGMDDLNNMINTVKSDCPDSTLLGTFFVENHDNPR 320
Db 241 PYQNVMDGVNLNPIYIYPLNNAFKSTSGMDDLNNMINTVKSDCPDSTLLGTFFVENHDNPR 300

QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSLYK 380

Db 301 FASYTNDIALAKNVAAPFIILNDGIPPIYAGOEQHYAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNVAISKDTGFTYKWNPIYKDD 411
Db 361 LIASANAIRNVAISKDTGFTYKWNPIYKDD 391

RESULT 13

US-10-815-495-22
; Sequence 22, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connelly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; TITLE OF INVENTION: Mutants Of Aspergillus Niger
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 22
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-22

Query Match 77.1%; Score 384; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAWWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGG 60
Db 2 MVAWWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGG 61
QY 61 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVGHYQWQDIYSLNENYGTTADDL 120
Db 62 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVGHYQWQDIYSLNENYGTTADDL 121
QY 121 KALSSALHERGMVLMVDVVAANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
Db 122 KALSSALHERGMVLMVDVVAANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181
QY 181 VEDCWLGDNVTSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVQKDFWPGYN 240
Db 182 VEDCWLGDNVTSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVQKDFWPGYN 241
QY 241 KAAGVYCIGEVLDGDPAYTCYQNVMDGVNLNPIYYPYLLNAPFKSTSGSMDLLYNNMINTVK 300
Db 242 KAAGVYCIGEVLDGDPAYTCYQNVMDGVNLNPIYYPYLLNAPFKSTSGSMDLLYNNMINTVK 301
QY 301 SDPCDSTLLGTFFVENHNDNPRFASYTNDIALAKNVAAPFIILNDGIPPIYAGOEQHYAGGND 360
Db 302 SDPCDSTLLGTFFVENHNDNPRFASYTNDIALAKNVAAPFIILNDGIPPIYAGOEQHYAGGND 361
QY 361 PANREATWLSGYPTDSELYKLIAS 384
Db 362 PANREATWLSGYPTDSELYKLIAS 385

RESULT 14

US-10-815-495-18
; Sequence 18, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connelly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; TITLE OF INVENTION: Mutants Of Aspergillus Niger
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495

; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 18
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-18

Query Match 77.1%; Score 384; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAWWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGG 60
Db 2 MVAWWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGG 61
QY 61 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVGHYQWQDIYSLNENYGTTADDL 120
Db 62 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVGHYQWQDIYSLNENYGTTADDL 121
QY 121 KALSSALHERGMVLMVDVVAANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
Db 122 KALSSALHERGMVLMVDVVAANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181
QY 181 VEDCWLGDNVTSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVQKDFWPGYN 240
Db 182 VEDCWLGDNVTSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVQKDFWPGYN 241
QY 241 KAAGVYCIGEVLDGDPAYTCYQNVMDGVNLNPIYYPYLLNAPFKSTSGSMDLLYNNMINTVK 300
Db 242 KAAGVYCIGEVLDGDPAYTCYQNVMDGVNLNPIYYPYLLNAPFKSTSGSMDLLYNNMINTVK 301
QY 301 SDPCDSTLLGTFFVENHNDNPRFASYTNDIALAKNVAAPFIILNDGIPPIYAGOEQHYAGGND 360
Db 302 SDPCDSTLLGTFFVENHNDNPRFASYTNDIALAKNVAAPFIILNDGIPPIYAGOEQHYAGGND 361
QY 361 PANREATWLSGYPTDSELYKLIAS 384
Db 362 PANREATWLSGYPTDSELYKLIAS 385

RESULT 15

US-10-228-063-45
; Sequence 45, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lanahan, Mike
; TITLE OF INVENTION: Self-processing Plants and Plant Parts
; FILE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Aspergillus shiroleusami
US-10-228-063-45

Query Match 75.7%; Score 377; DB 14; Length 1095;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 ATPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WTPVTAQLPQTAYGDVGHYQWQDIYSLNENYGTTADDL KALSSALHERGMVLMVDVVA 140
Db 61 WTPVTAQLPQTAYGDVGHYQWQDIYSLNENYGTTADDL KALSSALHERGMVLMVDVVA 120
QY 141 NEMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNVTSLPDLDTTK 200

Db	121	NHMGYDAGAGSYDYGVFPKPFSSQDYFHPFCIQNTYEDQTVQEDCWLGNDVNTSLPDLDTTK	180
Qy	201	DVVKNEWYDWSGLSVNSKYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCVIGEVLDDGPAYTC	260
Db	181	DVVKNEWYDWSGLSVNSKYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCVIGEVLDDVPAYTC	240
Qy	261	PYQNVMDGVLYNPYIYPYLLNAPKSTSGSMDDLYNNINTVKSCDPDSTLLGTFTVENHDNPR	320
Db	241	PYQNVMDGVLYNPYIYPYLLNAPKSTSGSMDDLYNNINTVKSCDPDSTLLGTFTVENHDNPR	300
Qy	321	FASYTNDIALAKNVAAFIILNDGIPILYAGQEQHYAGNDDPANREATWLSGYPTDSELYK	380
Db	301	FASYTNDIALAKNVAAFIILNDGIPILYAGQEQHYAGNDDPANREATWLSGYPTDSELYK	360
Qy	381	LIASANAIRNVAISKDTGFVTYKNWPIYKDDPTTIAMRKGTDCGSQVITVILSNKGASGDSYT	440
Db	361	LIASANAIRNVAISKDTGFVTYKNWPIYKDDPTTIAMRKGTDCGSQVITVILSNKGASGDSYT	420
Qy	441	LSLSGAGYTAGQQLTEVIGTCTTVTVSGDGNVPVPMAGGLPRVLYPTEKLAGSKI CSSS	498
Db	421	LSLSGAGYTAGQQLTEVIGTCTTVTVSGDGNVPVPMAGGLPRVLYPTEKLAGSKI CSSS	478

Search completed: November 7, 2005, 19:22:49
Job time : 267.305 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:45:18 ; Search time 74.9884 Seconds
(without alignments)
495.746 Million cell updates/sec

Title: US-10-820-200-2

Perfect score: 498
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Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	391	78.5	478	1	US-08-720-899-7
2	391	78.5	478	1	US-08-459-610-7
3	391	78.5	478	2	US-08-343-804-7
4	391	78.5	478	2	US-08-600-908A-10
5	391	78.5	478	3	US-08-683-838A-10
6	391	78.5	478	3	US-09-182-859-7
7	391	78.5	478	4	US-09-672-459-7
8	391	78.5	478	4	US-09-636-252A-10
9	391	78.5	478	4	US-10-186-042-7
10	238	47.8	478	2	US-08-339-715A-2
11	18	3.6	304	3	US-09-189-060B-72
12	18	3.6	306	3	US-09-189-060B-66
13	18	3.6	306	3	US-09-189-060B-68
14	18	3.6	307	3	US-09-189-060B-74
15	18	3.6	308	3	US-09-189-060B-70
16	11	2.2	468	1	US-08-204-656B-2
17	11	2.2	468	1	US-08-204-656B-4
18	11	2.2	468	1	US-08-204-656B-6
19	11	2.2	468	1	US-08-204-656B-8
20	11	2.2	468	1	US-08-470-702-6
21	11	2.2	468	1	US-08-470-702-7
22	11	2.2	468	1	US-08-470-702-8
23	11	2.2	468	1	US-08-470-702-9
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27	11	2.2	468	1	US-08-467-831-9

28 8 1.6 450 4 US-09-252-991A-25354 Sequence 25354, A
29 8 1.6 477 4 US-09-134-000C-4388 Sequence 4388, Ap
30 8 1.6 2039 4 US-09-077-098A-7 Sequence 7, Appli
31 7 1.4 22 3 US-09-613-182-7 Sequence 7, Appli
32 7 1.4 63 4 US-09-248-796A-25725 Sequence 25725, A
33 7 1.4 63 4 US-09-513-998C-4374 Sequence 4374, A
34 7 1.4 117 4 US-09-647-468-142 Sequence 142, App
35 7 1.4 119 4 US-09-647-468-30 Sequence 30, Appl
36 7 1.4 119 4 US-09-647-468-40 Sequence 40, Appl
37 7 1.4 119 4 US-09-647-468-42 Sequence 42, Appl
38 7 1.4 119 4 US-09-647-468-50 Sequence 50, Appl
39 7 1.4 119 4 US-09-647-468-52 Sequence 52, Appl
40 7 1.4 119 4 US-09-647-468-58 Sequence 58, Appl
41 7 1.4 119 4 US-09-647-468-60 Sequence 60, Appl
42 7 1.4 119 4 US-09-647-468-64 Sequence 64, Appl
43 7 1.4 119 4 US-09-647-468-70 Sequence 70, Appl
44 7 1.4 119 4 US-09-647-468-72 Sequence 72, Appl
45 7 1.4 119 4 US-09-647-468-76 Sequence 76, Appl

ALIGNMENTS

RESULT 1

US-08-720-899-7

; Sequence 7, Application US/08720899

; Patent No. 5753460

; GENERAL INFORMATION:

; APPLICANT: Bisgaard-Frantzen, Henrik

; APPLICANT: Borchert, Torben Vedel

; APPLICANT: Svendsen, Allan

; APPLICANT: Thellersen, Marianne

; APPLICANT: Van der Zee, Pia

; TITLE OF INVENTION: AMYLASE VARIANTS

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESSES:

; ADDRESSES: NO. 57534600 No. 5753460disk of No. 5753460ch America, Inc.

; STREET: 405 Lexington Avenue, 64th Floor

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA: US/08/720,899

; FILING DATE: 10-OCT-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/343,804

; FILING DATE: 22-NOV-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lowney Dr., Karen A.

; REGISTRATION NUMBER: 31,274

; REFERENCE/DOCKET NUMBER: 4054.214-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 478 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-720-899-7

Query Match 78.5%; Score 391; DB 1; Length 478;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-343-804-7

Query Match 78.5%; Score 391; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATPADWRSOSIYFLLTDRFARTDGTATCNTADQKYCGGTWQGIIDKLDYIQMGFTAI 60
Qy 81 WITPVTQAQLPQTAYGDAYHYGQWQDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
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Db 121 NMGYDGAGSSVDYVFKPFSSQDYFHPFCFIONYEDQTVQVDCWLGDNVSLPDLDTTK 180
Qy 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAAGVYCIGEVLDGDPAYTC 260
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Db 241 PQYNVMDGVLNPIYYPYLLNAPFKSTSGSMDLLNMINVTVKSDCPDSTLLGTFVENHDNPR 300
Qy 321 FASYTNDIALAKNVAAPFIINDGIPIIYAGQEOHYAGGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAPFIINDGIPIIYAGQEOHYAGGNDPANREATWLSGYPTDSELYK 360
Qy 381 LIASANAIRNAYAIKSDTGFVYKNWPIYKDD 411
Db 361 LIASANAIRNAYAIKSDTGFVYKNWPIYKDD 391

RESULT 4
US-08-600-908A-10
; Sequence 10, Application US/08600908A
; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: '-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5989169 No. 5989169disk of No. 5989169th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-600-908A-10

Query Match 78.5%; Score 391; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATPADWRSOSIYFLLTDRFARTDGTATCNTADQKYCGGTWQGIIDKLDYIQMGFTAI 60
Qy 81 WITPVTQAQLPQTAYGDAYHYGQWQDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
Db 61 WITPVTQAQLPQTAYGDAYHYGQWQDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120
Qy 141 NMGYDGAGSSVDYVFKPFSSQDYFHPFCFIONYEDQTVQVDCWLGDNVSLPDLDTTK 200
Db 121 NMGYDGAGSSVDYVFKPFSSQDYFHPFCFIONYEDQTVQVDCWLGDNVSLPDLDTTK 180
Qy 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAAGVYCIGEVLDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAAGVYCIGEVLDGDPAYTC 240
Qy 261 PQYNVMDGVLNPIYYPYLLNAPFKSTSGSMDLLNMINVTVKSDCPDSTLLGTFVENHDNPR 320
Db 241 PQYNVMDGVLNPIYYPYLLNAPFKSTSGSMDLLNMINVTVKSDCPDSTLLGTFVENHDNPR 300
Qy 321 FASYTNDIALAKNVAAPFIINDGIPIIYAGQEOHYAGGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAPFIINDGIPIIYAGQEOHYAGGNDPANREATWLSGYPTDSELYK 360
Qy 381 LIASANAIRNAYAIKSDTGFVYKNWPIYKDD 411
Db 361 LIASANAIRNAYAIKSDTGFVYKNWPIYKDD 391

RESULT 5
US-08-683-838A-10
; Sequence 10, Application US/08683838A
; Patent No. 6022724
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: '-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6022724 No. 6022724disk of No. 6022724th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,838A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-683-838A-10

Query Match 78.5%; Score 391; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATPADWRSQSIYFLLTDRPARTDGGTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTQALPQTAYGDAYHGYWQODIYSLNENYGTADDLKALSSALHERGMVLDVVA 140
DB 61 WITPVTQALPQTAYGDAYHGYWQODIYSLNENYGTADDLKALSSALHERGMVLDVVA 120
QY 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIONYEDQTVEDCWLGDNTVSLPDLDTTK 200
DB 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIONYEDQTVEDCWLGDNTVSLPDLDTTK 180
QY 201 DVVKNEWTDWVGLSVNSYSDGLRIDTVKHQKDFWPGYNKAAGVYCVIGEVLDDGDPAYTC 260
DB 181 DVVKNEWTDWVGLSVNSYSDGLRIDTVKHQKDFWPGYNKAAGVYCVIGEVLDDGDPAYTC 240
QY 261 PYQNMVDGVLNYPPIYPLLNAPKSTSGMDDLNNMINTVKSDCPDSTLLGTVEVHNHNP 320
DB 241 PYQNMVDGVLNYPPIYPLLNAPKSTSGMDDLNNMINTVKSDCPDSTLLGTVEVHNHNP 300
QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 380
DB 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNVAISKDTGFTYKNWPIYKDD 411
DB 361 LIASANAIRNVAISKDTGFTYKNWPIYKDD 391

RESULT 6

US-09-182-859-7
; Sequence 7, Application US/09182859
; Patent No. 6143708
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/182,859
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: 0515/96
; EARLIER FILING DATE: 1996-04-30
; EARLIER APPLICATION NUMBER: 0712/96
; EARLIER FILING DATE: 1996-06-28
; EARLIER APPLICATION NUMBER: 0775/96
; EARLIER FILING DATE: 1996-07-11
; EARLIER APPLICATION NUMBER: 1263/96
; EARLIER FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-182-859-7

Query Match 78.5%; Score 391; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRPARTDGGTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
DB 1 ATPADWRSQSIYFLLTDRPARTDGGTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTQALPQTAYGDAYHGYWQODIYSLNENYGTADDLKALSSALHERGMVLDVVA 140
DB 61 WITPVTQALPQTAYGDAYHGYWQODIYSLNENYGTADDLKALSSALHERGMVLDVVA 120
QY 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIONYEDQTVEDCWLGDNTVSLPDLDTTK 200
DB 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIONYEDQTVEDCWLGDNTVSLPDLDTTK 180
QY 201 DVVKNEWTDWVGLSVNSYSDGLRIDTVKHQKDFWPGYNKAAGVYCVIGEVLDDGDPAYTC 260
DB 181 DVVKNEWTDWVGLSVNSYSDGLRIDTVKHQKDFWPGYNKAAGVYCVIGEVLDDGDPAYTC 240
QY 261 PYQNMVDGVLNYPPIYPLLNAPKSTSGMDDLNNMINTVKSDCPDSTLLGTVEVHNHNP 320
DB 241 PYQNMVDGVLNYPPIYPLLNAPKSTSGMDDLNNMINTVKSDCPDSTLLGTVEVHNHNP 300
QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 380
DB 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNVAISKDTGFTYKNWPIYKDD 411
DB 361 LIASANAIRNVAISKDTGFTYKNWPIYKDD 391

RESULT 7

US-09-672-459-7
; Sequence 7, Application US/09672459
; Patent No. 6436888
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/672,459
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-672-459-7

Query Match 78.5%; Score 391; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATPADWRSQSIYFLLTDRPARTDGGTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTQALPQTAYGDAYHGYWQODIYSLNENYGTADDLKALSSALHERGMVLDVVA 140

Db 61 WITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 120
QY 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNDNTVSLPDLDTTK 200
Db 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNDNTVSLPDLDTTK 180
QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
QY 261 PYQNVMDGVNLPIIYVPLNAPKSTSGSMDLLYNMINTVKS DCPDSTLLGTFFVENHDNPR 320
Db 241 PYQNVMDGVNLPIIYVPLNAPKSTSGSMDLLYNMINTVKS DCPDSTLLGTFFVENHDNPR 300
QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQHQHVGAGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQHQHVGAGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNVAISKDTGFTVTKNMPYKDD 411
Db 361 LIASANAIRNVAISKDTGFTVTKNMPYKDD 391

RESULT 8

US-09-636-252A-10
; Sequence 10, Application US/09636252A
; Patent No. 6440716
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1P216-US2
; CURRENT APPLICATION NUMBER: US/09/636,252A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1998-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-09-636-252A-10

Query Match 78.5%; Score 391; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 ATPADWRSQSIYFLLTDRFARTDGSSTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 140
Db 61 WITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 120
QY 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNDNTVSLPDLDTTK 200
Db 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNDNTVSLPDLDTTK 180
QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
QY 261 PYQNVMDGVNLPIIYVPLNAPKSTSGSMDLLYNMINTVKS DCPDSTLLGTFFVENHDNPR 320
Db 241 PYQNVMDGVNLPIIYVPLNAPKSTSGSMDLLYNMINTVKS DCPDSTLLGTFFVENHDNPR 300
QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQHQHVGAGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQHQHVGAGNDPANREATWLSGYPTDSELYK 360

QY 381 LIASANAIRNVAISKDTGFTVTKNMPYKDD 411
Db 361 LIASANAIRNVAISKDTGFTVTKNMPYKDD 391

RESULT 9

US-10-186-042-7
; Sequence 7, Application US/10186042
; Patent No. 6642044
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match 78.5%; Score 391; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 ATPADWRSQSIYFLLTDRFARTDGSSTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 140
Db 61 WITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 120
QY 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNDNTVSLPDLDTTK 200
Db 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNDNTVSLPDLDTTK 180
QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
QY 261 PYQNVMDGVNLPIIYVPLNAPKSTSGSMDLLYNMINTVKS DCPDSTLLGTFFVENHDNPR 320
Db 241 PYQNVMDGVNLPIIYVPLNAPKSTSGSMDLLYNMINTVKS DCPDSTLLGTFFVENHDNPR 300
QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQHQHVGAGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQHQHVGAGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNVAISKDTGFTVTKNMPYKDD 411
Db 361 LIASANAIRNVAISKDTGFTVTKNMPYKDD 391

RESULT 10

US-08-339-715A-2
; Sequence 2, Application US/08339715A

; Patent No. 5965442
; GENERAL INFORMATION:
; APPLICANT: Kaneko, Hiroki
; APPLICANT: Takada, Toshikazu
; APPLICANT: Shimada, Jiro
; APPLICANT: Kuriki, Takashi
; APPLICANT: Yanase, Michio
; APPLICANT: Takata, Hiroki
; APPLICANT: Okada, Shigetaka
; TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
; TITLE OF INVENTION: NEOPULLULANASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: POHAM, HAIK, SCHNOBICH & KAUFMAN, LTD.
; STREET: Metropolitan Square Building, Suite 800, 1450
; STREET: G. Street
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,715A
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306096/1993
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Welser, Allen S.
; REGISTRATION NUMBER: 27,215
; REFERENCE/DOCKET NUMBER: 18335.009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-824-8000
; TELEFAX: 202-824-8199
; TELEX: 248516
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-339-715A-2

Query Match 47.8%; Score 238; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.1e-219; Mismatches 0; Indels 0; Gaps 0;
Matches 238; Conservative 0;
QY 106 DIYSLNENYGTADDLKALSSALHERGMYLMDVVDVVAHNGYDAGSSVDYSVFKPSSQDY 165
DB |||||||
86 DIYSLNENYGTADDLKALSSALHERGMYLMDVVDVVAHNGYDAGSSVDYSVFKPSSQDY 145
QY 166 FHPFCFIQNYEDOTQVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYSDGLRI 225
DB |||||||
146 FHPFCFIQNYEDQTVQEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYSDGLRI 205
QY 226 DTVKHVQKDFWPGYKAAAGVYICIGVLGDPAITCPYQNVMDGVNLNPIYYPLLNAPKST 285
DB |||||||
206 DTVKHVQKDFWPGYKAAAGVYICIGVLGDPAITCPYQNVMDGVNLNPIYYPLLNAPKST 265
QY 286 SGSMDDLNNMINTVKSCDPDSTLLGTFFVENHDNPRFASVYNDIALAKNVAAFIILNDG 343
DB |||||||
266 SGSMDDLNNMINTVKSCDPDSTLLGTFFVENHDNPRFASVYNDIALAKNVAAFIILNDG 323

RESULT 11
US-09-189-060B-72
; Sequence 72, Application US/09189060B

; Patent No. 6270968
; GENERAL INFORMATION:
; APPLICANT: Dalboge, Henrik
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Markus
; APPLICANT: Borge, Diderichsen
; TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
; FILE REFERENCE: 4772.204-US
; CURRENT APPLICATION NUMBER: US/09/189,060B
; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/DK97/00216
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Hybrid
; US-09-189-060B-72

Query Match 3.6%; Score 18; DB 3; Length 304;
Best Local Similarity 100.0%; Pred. No. 6.2e-09; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 1 MVAWMSFLYGLQVAAPA 18
DB |||||||
2 MVAWMSFLYGLQVAAPA 19
DB |||||||

RESULT 12
US-09-189-060B-66
; Sequence 66, Application US/09189060B
; Patent No. 6270968
; GENERAL INFORMATION:
; APPLICANT: Dalboge, Henrik
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Markus
; APPLICANT: Borge, Diderichsen
; TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
; FILE REFERENCE: 4772.204-US
; CURRENT APPLICATION NUMBER: US/09/189,060B
; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/DK97/00216
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Hybrid
; US-09-189-060B-66

Query Match 3.6%; Score 18; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 6.2e-09; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 1 MVAWMSFLYGLQVAAPA 18
DB |||||||
4 MVAWMSFLYGLQVAAPA 21
DB |||||||

RESULT 13
US-09-189-060B-68
; Sequence 68, Application US/09189060B
; Patent No. 6270968
; GENERAL INFORMATION:
; APPLICANT: Dalboge, Henrik
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Markus
; APPLICANT: Borge, Diderichsen
; TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
; FILE REFERENCE: 4772.204-US
; CURRENT APPLICATION NUMBER: US/09/189,060B

; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/DK97/00216
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Hybrid
US-09-189-060B-68

Query Match 3.6%; Score 18; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAWMSFLYGLQVAAPA 18
| | | | | | | | | | | | | | | | | | | | | |
DB 4 MVAWMSFLYGLQVAAPA 21
| | | | | | | | | | | | | | | | | | | | | |

RESULT 14
US-09-189-060B-74
; Sequence 74, Application US/09189060B
; Patent No. 6270968
; GENERAL INFORMATION:
; APPLICANT: Dalboge, Henrik
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Markus
; APPLICANT: Borge, Diderichsen
; TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
; FILE REFERENCE: 4772.204-US
; CURRENT APPLICATION NUMBER: US/09/189,060B
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/DK97/00216
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Hybrid
US-09-189-060B-74

Query Match 3.6%; Score 18; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 6.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAWMSFLYGLQVAAPA 18
| | | | | | | | | | | | | | | | | | | | | |
DB 4 MVAWMSFLYGLQVAAPA 21
| | | | | | | | | | | | | | | | | | | | | |

RESULT 15
US-09-189-060B-70
; Sequence 70, Application US/09189060B
; Patent No. 6270968
; GENERAL INFORMATION:
; APPLICANT: Dalboge, Henrik
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Markus
; APPLICANT: Borge, Diderichsen
; TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
; FILE REFERENCE: 4772.204-US
; CURRENT APPLICATION NUMBER: US/09/189,060B
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/DK97/00216
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Hybrid

US-09-189-060B-70

Query Match 3.6%; Score 18; DB 3; Length 308;
Best Local Similarity 100.0%; Pred. No. 6.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAWMSFLYGLQVAAPA 18
| | | | | | | | | | | | | | | | | | | | | |
DB 4 MVAWMSFLYGLQVAAPA 21
| | | | | | | | | | | | | | | | | | | | | |

Search completed: November 7, 2005, 19:00:08
Job time : 75.9884 secs

1950-1951 (1950-1951)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 19:15:40 ; Search time 60.5676 Seconds
(without alignments)
791.116 Million cell updates/sec

Title: US-10-820-200-2
Perfect score: 498
Sequence: 1 MWAWNSLFYGLQVAAPALA.....LPRVLYPTKLAGSKICSSS 498

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 79;*

1: Pir1: *
2: Pir2: *
3: Pir3: *
4: Pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	100.0	499	1 ALAS1	alpha-amylase (EC
2	397	79.7	499	2 JS0663	alpha-amylase (EC
3	384	77.1	498	2 A48305	alpha-amylase (EC
4	384	77.1	499	2 B48305	alpha-amylase (EC
5	342	68.7	499	1 ALAS3	alpha-amylase (EC
6	296	59.4	499	2 JN0588	alpha-amylase (EC
7	244	49.0	499	2 JT0466	alpha-amylase (EC
8	238	47.8	478	2 JK0201	alpha-amylase (EC
9	20	4.0	507	2 S33921	alpha-amylase (EC
10	19	3.8	512	2 S23355	alpha-amylase (EC
11	19	3.8	512	2 S06115	alpha-amylase (EC
12	19	3.8	513	2 T38770	alpha-amylase a pr
13	16	3.2	624	1 JC4510	pullulanase (EC 3.
14	14	2.8	484	1 A35282	alpha-amylase (EC
15	12	2.4	482	2 S31478	alpha-amylase (EC
16	12	2.4	1196	2 A29130	beta-amylase (EC 3
17	11	2.2	494	1 ALBYAF	alpha-amylase (EC
18	10	2.0	625	2 T41603	alpha-amylase - fi
19	10	2.0	631	2 S72270	alpha-amylase (EC
20	9	1.8	581	2 S62505	probable alpha-am
21	8	1.6	140	2 H75368	hypothetical prote
22	8	1.6	149	2 G87329	hypothetical prote
23	8	1.6	151	2 A86695	hypothetical prote
24	8	1.6	160	2 E72529	hypothetical prote
25	8	1.6	258	2 C70968	probable ribD - My
26	8	1.6	305	2 H83344	hypothetical prote
27	8	1.6	326	2 C82200	cytochrome c oxida
28	8	1.6	494	1 A25529	alpha-amylase (EC
29	8	1.6	494	2 S58964	alpha-amylase (EC

30	8	1.6	494	2 S58960	alpha-amylase (EC
31	8	1.6	494	2 S58962	alpha-amylase (EC
32	8	1.6	494	2 S58953	alpha-amylase (EC
33	8	1.6	494	2 S58956	alpha-amylase (EC
34	8	1.6	494	2 S58958	alpha-amylase (EC
35	8	1.6	494	2 S58957	alpha-amylase (EC
36	8	1.6	494	2 S58965	alpha-amylase (EC
37	8	1.6	494	2 S58951	alpha-amylase (EC
38	8	1.6	494	2 S58954	alpha-amylase (EC
39	8	1.6	494	2 A60766	alpha-amylase (EC
40	8	1.6	623	2 T35377	probable membrane
41	8	1.6	690	2 B82409	alpha-amylase VCA0
42	8	1.6	774	2 T39539	alpha-amylase homo
43	8	1.6	829	2 E87305	TonB-dependent rec
44	8	1.6	919	2 S28179	alpha-amylase (EC
45	8	1.6	1036	2 AG1326	alpha-mannosidase

ALIGNMENTS

RESULT 1

ALAS1

alpha-amylase (EC 3.2.1.1) 1 precursor [validated] - Aspergillus oryzae

N:Alternate names: alpha-amylase isozyme II; glycogenase; Taka-amylase A

C:Species: Aspergillus oryzae

C>Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004

C:Accession: S04548; A33214; JS0240; A91930; A93767; A10627

R:Wirsal, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.

Mol. Microbiol. 3, 3-14, 1989

A:Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon

A:Reference number: S04548; MUID:89237897; PMID:2785629

A:Accession: S04548

A:Molecule type: DNA

A:Residues: 1-499 <WIR>

A:Cross-references: UNIPROT:P10529; EMBL:X12725; NID:G2430; PIDN:CAA31218.1; PID:G29592

A:Genetics: AMY1

A:Accession: A33214

A:Molecule type: mRNA

A:Residues: 1-499 <W12>

A:Cross-references: GB:X12725; NID:G2430; PIDN:CAA31218.1; PID:G295921

R:Genes, M.J.; Dove, M.J.; Seligy, V.L.

Gene 79, 107-117, 1989

A:Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containin

A:Reference number: JS0240; MUID:89378767; PMID:2789162

A:Accession: JS0240

A:Molecule type: DNA

A:Residues: 1-499 <GEN>

A:Genetics: AMY2

A>Note: the authors refer to this as isozyme II

R:Rifemura, S.; Ikenaka, T.

J. Biochem. 74, 1-10, 1973

A:Reference number: A91930; MUID:74001521; PMID:4733850

A:Accession: A91930

A:Molecule type: protein

A:Residues: 206-225 <ISE>

R:Narita, K.

Proc. Jpn. Acad. 51, 285-290, 1975

A:Reference number: A93767

A:Accession: A93767

A:Molecule type: protein

A:Residues: 434-443,446-447, 'Q',449-458, 'G'NTV',459-464,467-468, 'B',470, 'B',472-499 <NAR

R:Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.

J. Biochem. 95, 697-702, 1984

A:Title: Structure and possible catalytic residues of Taka-amylase A.

A:Reference number: A37454; MUID:84212370; PMID:6609921

A:Contents: annotation; X-ray crystallography, 3.0 angstroms

R:Swift, H.J.; Brady, L.; Derewenda, Z.S.; Dodson, E.J.; Turkmenburg, J.P.; Wilkinson, A.

submitted to the Brookhaven Protein Data Bank, August 1992

A:Reference number: A51548; PDB:6TAA

A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 22-497

C:Comment: One atom of calcium per molecule is essential for activity.

C:Genetics: <AMY1>

A:Gene: amy1
A:Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C:Genetics: <AMY2>
A:Gene: amy2; AmyII
A:Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <SIG>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
F:142,183,196,231/Binding site: calcium (Asn, Glu, His) #status predicted
F:218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:227,251,318/Active site: Asp, Glu, Asp #status predicted

Query Match	100.0%;	Score 498;	DB 1;	Length 499;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 498;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAPADWRQSISYFLLTDRFARTDGGSTTATCNTADOKYCGG 60
DB 2 MVAMWSFLYGLQVAAPALAAPADWRQSISYFLLTDRFARTDGGSTTATCNTADOKYCGG 61
QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL 121
QY 121 KALSSALHERGMYLMDVVANHMGYDGGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
DB 122 KALSSALHERGMYLMDVVANHMGYDGGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181
QY 181 VEDCWLGNTVSLPDLDTTKDVVKNWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPFGYN 240
DB 182 VEDCWLGNTVSLPDLDTTKDVVKNWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPFGYN 241
QY 241 KAAGYVICGEVLDDGPATPCYQNVMDGLVNLPIYYPILLNAPKSTGSMDDLNNMINTVK 300
DB 242 KAAGYVICGEVLDDGPATPCYQNVMDGLVNLPIYYPILLNAPKSTGSMDDLNNMINTVK 301
QY 301 SDPCPSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAFIILNDGIPILYAGQEHYAGGND 360
DB 302 SDPCPSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAFIILNDGIPILYAGQEHYAGGND 361
QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 420
DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 421
QY 421 DGSQIVTILSNKGASGDSYTLSSLGAGYTAGQQLTEVIGCTTGTGSDGNVPVPMAGGLP 480
DB 422 DGSQIVTILSNKGASGDSYTLSSLGAGYTAGQQLTEVIGCTTGTGSDGNVPVPMAGGLP 481
QY 481 RVLYPEKLAGSKICSSS 498
DB 482 RVLYPEKLAGSKICSSS 499

RESULT 2
JS0663
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus sp.
C:Species: Aspergillus sp.
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
C:Accession: JS0663
R:Shibuya, I.; Tamura, G.; Ishikawa, T.; Hara, S.
Biosci. Biotechnol. Biochem. 56, 174-179, 1992
A:Title: Cloning of the alpha-amylase cDNA of Aspergillus shiroyamii and its expression
A:Reference number: JS0663; MUID:92323146; PMID:1368777
A:Accession: JS0663
A:Molecule type: mRNA
A:Residues: 1-499 <SHI>
C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <SIG>
F:122-499/Product: alpha-amylase #status predicted <ALP>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	79.7%;	Score 397;	DB 2;	Length 499;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 497;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAPADWRQSISYFLLTDRFARTDGGSTTATCNTADOKYCGG 60
DB 2 MVAMWSFLYGLQVAAPALAAPADWRQSISYFLLTDRFARTDGGSTTATCNTADOKYCGG 61
QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL 121
QY 121 KALSSALHERGMYLMDVVANHMGYDGGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
DB 122 KALSSALHERGMYLMDVVANHMGYDGGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181
QY 181 VEDCWLGNTVSLPDLDTTKDVVKNWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPFGYN 240
DB 182 VEDCWLGNTVSLPDLDTTKDVVKNWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPFGYN 241
QY 241 KAAGYVICGEVLDDGPATPCYQNVMDGLVNLPIYYPILLNAPKSTGSMDDLNNMINTVK 300
DB 242 KAAGYVICGEVLDDGPATPCYQNVMDGLVNLPIYYPILLNAPKSTGSMDDLNNMINTVK 301
QY 301 SDPCPSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAFIILNDGIPILYAGQEHYAGGND 360
DB 302 SDPCPSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAFIILNDGIPILYAGQEHYAGGND 361
QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 420
DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 421
QY 421 DGSQIVTILSNKGASGDSYTLSSLGAGYTAGQQLTEVIGCTTGTGSDGNVPVPMAGGLP 480
DB 422 DGSQIVTILSNKGASGDSYTLSSLGAGYTAGQQLTEVIGCTTGTGSDGNVPVPMAGGLP 481
QY 481 RVLYPEKLAGSKICSSS 498
DB 482 RVLYPEKLAGSKICSSS 499

RESULT 3
A48305
alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori
C:Species: Aspergillus awamori
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: A48305
R:Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A:Title: Cloning, characterization, and expression of two alpha-amylase genes from Asper
A:Reference number: A48305; MUID:90254827; PMID:2340591
A:Accession: A48305
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-498 <KOR>
C:Cross-references: UNIPROT:Q02905
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:194-321/Domain: alpha-amylase core homology <AMY>

Query Match	77.1%;	Score 384;	DB 2;	Length 498;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYAWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGTATCNTADQKCGG 60
DB 2 MYAWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGTATCNTADQKCGG 61
QY 61 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHYGQWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHYGQWQDIYSLNENYGTADDL 121
QY 121 KALSSALHERGMVLMVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFQNYEDQTO 180
DB 122 KALSSALHERGMVLMVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFQNYEDQTO 181
QY 181 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGLSVNSYIDGLRIDTVKHVKQDFWPGYN 240
DB 182 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGLSVNSYIDGLRIDTVKHVKQDFWPGYN 241
QY 241 KAAGVYCIGEVLDGDPAYTCPPYQNVMDGVLNPIYIYPLLNAPFKSTSGSMDDLYNMINTVK 300
DB 242 KAAGVYCIGEVLDGDPAYTCPPYQNVMDGVLNPIYIYPLLNAPFKSTSGSMDDLYNMINTVK 301
QY 301 SDCPDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGQSOHYAGGND 360
DB 302 SDCPDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGQSOHYAGGND 361
QY 361 PANREATWLSGYPTDSELYKLIAS 384
DB 362 PANREATWLSGYPTDSELYKLIAS 385

RESULT 4
B48305
alpha-amylase (EC 3.2.1.1) B precursor - Aspergillus awamori
C:Species: Aspergillus awamori
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: B48305
R:Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A>Title: Cloning, characterization, and expression of two alpha-amylase genes from Asper
A:Reference number: A48305; MUID:190254827; PMID:2340591
A:Accession: B48305
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-499 <KOR>
A:Cross-references: UNIPROT:Q02906
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:194-321/Domain: alpha-amylase core homology <AMY>

Query Match 77.1%; Score 384; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYAWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGTATCNTADQKCGG 60
DB 2 MYAWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGTATCNTADQKCGG 61
QY 61 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHYGQWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHYGQWQDIYSLNENYGTADDL 121
QY 121 KALSSALHERGMVLMVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFQNYEDQTO 180
DB 122 KALSSALHERGMVLMVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFQNYEDQTO 181
QY 181 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGLSVNSYIDGLRIDTVKHVKQDFWPGYN 240
DB 182 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGLSVNSYIDGLRIDTVKHVKQDFWPGYN 241

QY 241 KAAGVYCIGEVLDGDPAYTCPPYQNVMDGVLNPIYIYPLLNAPFKSTSGSMDDLYNMINTVK 300
DB 242 KAAGVYCIGEVLDGDPAYTCPPYQNVMDGVLNPIYIYPLLNAPFKSTSGSMDDLYNMINTVK 301
QY 301 SDCPDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGQSOHYAGGND 360
DB 302 SDCPDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGQSOHYAGGND 361
QY 361 PANREATWLSGYPTDSELYKLIAS 384
DB 362 PANREATWLSGYPTDSELYKLIAS 385

RESULT 5
ALAS3
alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae
N:Alternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A
C:Species: Aspergillus oryzae
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S04549; A33215; A44713
R:Wirsael, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A>Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon
A:Reference number: S04548; MUID:89237897; PMID:2785629
A:Accession: S04549
A:Molecule type: DNA
A:Residues: 1-499 <WIR>
A:Cross-references: UNIPROT:Q96TH4; EMBL:X12727; NID:G2454; PIDN:CAA31220.1; PID:G29592.
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-499 <WI2>
R:Genes, M.J.; Dove, M.J.; Seligy, V.L.
Gene 79, 107-117, 1989
A>Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containin
A:Reference number: J50240; MUID:89378767; PMID:2789162
A:Accession: A44713
A:Molecule type: DNA
A:Residues: 1-499 <GEN>
A>Note: the authors refer to this as isozyme I
R:Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
A>Title: Structure and possible catalytic residues of Taka-amylase A.
A:Reference number: A37454; MUID:84212370; PMID:6609921
A:Contents: annotation; X-ray crystallography, 3.0 angstroms
C:Comment: One atom of calcium per molecule is essential for activity.
C:Genetics:
A:Gene: amy3; Amy1
A:Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; meta
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-499/Product: alpha-amylase 3 #status experimental <MAT>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
F:142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
F:218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:231,251,318/Active site: His, Glu, Asp #status experimental

Query Match 68.7%; Score 342; DB 1; Length 499;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 442; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 56 KYCGGTWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHYGQWQDIYSLNENY 115
DB 57 KYCGGTWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHYGQWQDIYSLNENY 116
QY 116 TADDLKALSSALHERGMVLMVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFQNY 175

Db	117	TADDLKALSSALHERGMVLMVDVANHMGYDCAGSSVDYSVEKPFSSQDYFHPFCLIQNY	176
Qy	176	EDQTOVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKVKQDF	235
Db	177	EDQTOVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKVKQDF	236
Qy	236	WFGYNKAAGVYICIGEVLDGDPAYTCPYQNVMDGVLNPIIYPLLNAPKSTSGSMDLNNM	295
Db	237	WFGYNKAAGVYICIGEVLDGDPAYTCPYQNVMDGVLNPIIYPLLNAPKSTSGSMDLNNM	296
Qy	296	INTVKSDDCPDSTLLGTGFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPPIIYAGOEQHY	355
Db	297	INTVKSDDCPDSTLLGTGFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPPIIYAGOEQHY	356
Qy	356	AGGNDPANREATWLSGYPTDSELYKLIIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIA	415
Db	357	AGGNDPANREATWLSGYPTDSELYKLIIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIA	416
Qy	416	MRKGTGSGQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPM	475
Db	417	MRKGTGSGQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPM	476
Qy	476	AGGLPRVLYPTEKLAGSKICSSS	498
Db	477	AGGLPRVLYPTEKLAGSKICSSS	499
RESULT 6			
JN0588			
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae			
N:Alternate names: Taka-amylase A			
C:Species: Aspergillus oryzae			
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004			
C:Accession: JN0588			
R:Tsukagoshi, N.; Furukawa, M.; Nagaba, H.; Kirita, N.; Tsuboi, A.; Udaka, S.			
Gene 84, 319-327, 1989			
A:Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for mu			
A:Reference number: JN0588; PMID:90128276; PMID:5612911			
A:Accession: JN0588			
A:Molecule type: mRNA			
A:Residues: 1-499 <TSU>			
A:Cross-references: UNIPROT:Q96TH4			
C:Comment: The alpha amylases are encoded by multigene family.			
C:Genetics:			
A:Gene: Taa-G1			
A:Introns: 56/1; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3			
C:Function:			
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds			
A:Pathway: glycogen/starch degradation			
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology			
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation			
F:1-21/Domain: signal sequence #status predicted <SIG>			
F:194-321/Product: alpha-amylase #status predicted <WAT>			
F:22-499/Product: alpha-amylase #status predicted <AMY>			
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted			
Query Match 59.4%; Score 296; DB 2; Length 499;			
Best Local Similarity 99.6%; Pred. No. 3.8e-294;			
Matches 496; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	1	MVAMWSFLYGLQVAAPALAAPDWRQSIFLLITDRFARTDGSSTTATCNTADQKCGG	60
Db	2	MVAMWSFLYGLQVAAPALAAPDWRQSIFLLITDRFARTDGSSTTATCNTADQKCGG	61
Qy	61	TWQGIIDKLDYIQMGFTAIWITPTVAQLPQTAYGDAYHGWQDIYSLNENYGTADDL	120
Db	62	TWQGIIDKLDYIQMGFTAIWITPTVAQLPQTAYGDAYHGWQDIYSLNENYGTADDL	121
Qy	121	KALSSALHERGMVLMVDVANHMGYDAGSSVDYSVEKPFSSQDYFHPFCLIQNYEDQTQ	180
Db	122	KALSSALHERGMVLMVDVANHMGYDAGSSVDYSVEKPFSSQDYFHPFCLIQNYEDQTQ	181

Qy	181	VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKVKQDFWPGYN	240
Db	182	VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKVKQDFWPGYN	241
Qy	241	KAAGVYICIGEVLDGDPAYTCPYQNVMDGVLNPIIYPLLNAPKSTSGSMDLNNINTVK	300
Db	242	KAAGVYICIGEVLDGDPAYTCPYQNVMDGVLNPIIYPLLNAPKSTSGSMDLNNINTVK	301
Qy	301	SDCPDSTLLGTGFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPPIIYAGOEQHYAGND	360
Db	302	SDCPDSTLLGTGFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPPIIYAGOEQHYAGND	361
Qy	361	PANREATWLSGYPTDSELYKLIIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRKT	420
Db	362	PANREATWLSGYPTDSELYKLIIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRKT	421
Qy	421	DGSGQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP	480
Db	422	DGSGQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP	481
Qy	481	RVLYPTEKLAGSKICSSS	498
Db	482	RVLYPTEKLAGSKICSSS	499
RESULT 7			
JT0466			
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae			
N:Alternate names: glycogenase; Taka-amylase A			
C:Species: Aspergillus oryzae			
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004			
C:Accession: JT0466			
R:Tada, S.; Iimura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.			
Agric. Biol. Chem. 53, 593-599, 1989			
A:Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergill			
A:Reference number: JT0466			
A:Accession: JT0466			
A:Molecule type: DNA			
A:Residues: 1-499 <TAD>			
A:Cross-references: UNIPROT:P10529			
C:Comment: See also PIR:JK0201 and PIR:JS0240.			
C:Comment: One atom of calcium per molecule is essential for activity.			
C:Genetics:			
A:Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3			
C:Function:			
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds			
A:Pathway: glycogen/starch degradation			
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology			
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation			
F:1-21/Domain: signal sequence #status predicted <SIG>			
F:22-499/Product: alpha-amylase #status predicted <MAT>			
F:194-321/Domain: alpha-amylase core homology <AMY>			
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted			
F:231,251,318/Active site: His, Glu, Asp #status predicted			
Query Match 49.0%; Score 244; DB 2; Length 499;			
Best Local Similarity 100.0%; Pred. No. 5.7e-241;			
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	255	DPAYTCPYQNVMDGVLNPIIYPLLNAPKSTSGSMDLNNINTVKSDCPDSTLLGTGTFVE	314
Db	256	DPAYTCPYQNVMDGVLNPIIYPLLNAPKSTSGSMDLNNINTVKSDCPDSTLLGTGTFVE	315
Qy	315	NHDNPRFASVTNDIALAKNVAAPFIILNDGIPPIIYAGOEQHYAGNDPANREATWLSGYPT	374
Db	316	NHDNPRFASVTNDIALAKNVAAPFIILNDGIPPIIYAGOEQHYAGNDPANREATWLSGYPT	375
Qy	375	DSELYKLIIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRKTGDSQVTTILSNKGA	434
Db	376	DSELYKLIIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRKTGDSQVTTILSNKGA	435
Qy	435	SGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKI	494

Db 436 SGDSYTLISGAGYTAGQQLTEVIGCTTTVSGDGNVPMAGGLPRVLPTKLAGSKI 495

QY 495 CSSS 498

Db 496 CSSS 499

RESULT 8

JK0201
alpha-amylase (EC 3.2.1.1) - Aspergillus oryzae
N:Alternate names: glycogenase; Taka-amylase A
C:Species: Aspergillus oryzae
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: JK0201
R:Toda, H.; Kondo, K.; Narita, K.
Proc. Jpn. Acad. 58B, 208-212, 1982
A:Title: The complete amino acid sequence of Taka-amylase A.
A:Reference number: JK0201
A:Accession: JK0201
A:Molecule type: protein
A:Residues: 1-478 <TOD>
A:Cross-references: UNIPROT:P10529
C:Comment: One atom of calcium per molecule is essential for the activity.
C:Comment: This enzyme is a glycoprotein.
C:Comment: See also PIR:J70466 and PIR:J50240.
C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:173-300/Domain: alpha-amylase core homology <AMY>
F:197/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:210,230,297/Active site: His, Glu, Asp #status experimental

Query Match 47.8%; Score 238; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 7.6e-235;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 DIYSLNENYGTADDKALSSALHERGMVLMVDVNVANHMGYDAGSSVDYVFKPSSQDY 165

Db 86 DIYSLNENYGTADDKALSSALHERGMVLMVDVNVANHMGYDAGSSVDYVFKPSSQDY 145

QY 166 FHPFCFIQNYEQTVEDCWLGDNTVSLPDLDTTKDVKVNEWYDVGSLVSNYSIDGLRI 225

Db 146 FHPFCFIQNYEQTVEDCWLGDNTVSLPDLDTTKDVKVNEWYDVGSLVSNYSIDGLRI 205

QY 226 DTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPATCTPQNVMDGVNLNPIYYPLLNAFKST 285

Db 206 DTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPATCTPQNVMDGVNLNPIYYPLLNAFKST 265

QY 286 SGSMDDLYNMINTVKSDCPDSTLLGTFFVENHDNPRFASVTNDIALAKNVAAFIILNDG 343

Db 266 SGSMDDLYNMINTVKSDCPDSTLLGTFFVENHDNPRFASVTNDIALAKNVAAFIILNDG 323

RESULT 9

S33921
alpha-amylase (EC 3.2.1.1) SWA2 precursor - yeast (Schwanniomyces occidentalis)
N:Alternate names: alpha-1,4 glucanohydrolase
C:Species: Schwanniomyces occidentalis
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: S33921
R:Claros, M.G.; Abarca, D.; Fernandez-Lobato, M.; Jimenez, A.
Curr. Genet. 24, 75-83, 1993
A:Title: Molecular structure of the SWA2 gene encoding an AMY1-related alpha-amylase from Schwanniomyces occidentalis
A:Reference number: S33921; MUID:93365041; PMID:8358835
A:Accession: S33921
A:Molecule type: DNA
A:Residues: 1-507 <CLA>
A:Cross-references: UNIPROT:Q08806; EMBL:X73497; NID:g396561; PID:g3965

C:Gene: SWA2

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-507/Product: alpha-amylase #status predicted <MAT>
F:205-332/Domain: alpha-amylase core homology <AMY>
F:134,229/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 4.0%; Score 20; DB 2; Length 507;
Best Local Similarity 100.0%; Pred. No. 7.4e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 QGIIDKLDYIQGMGFTAIWI 82

Db 75 QGIIDKLDYIQGMGFTAIWI 94

RESULT 10

S23355
alpha-amylase (EC 3.2.1.1) precursor - yeast (Schwanniomyces occidentalis)
C:Species: Schwanniomyces occidentalis
C>Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S23355
R:Wu, F.M.; Wang, T.T.; Heu, W.H.
FEMS Microbiol. Lett. 82, 313-318, 1991
A:Title: The nucleotide sequence of Schwanniomyces occidentalis alpha-amylase gene.
A:Reference number: S23355
A:Accession: S23355
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-512 <WUF>
A:Cross-references: UNIPROT:P19269; EMBL:X62079; NID:g4880; PID:CAA33995.1; PID:g4881
A:Note: The authors translated the codon AGA for residue 21 as Pro, CTT for residue 61
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase
F:209-336/Domain: alpha-amylase core homology <AMY>

Query Match 3.8%; Score 19; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 7.8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GIIDKLDYIQGMGFTAIWI 82

Db 80 GIIDKLDYIQGMGFTAIWI 98

RESULT 11

S06115
alpha-amylase (EC 3.2.1.1) AMY1 precursor - yeast (Schwanniomyces occidentalis)
C:Species: Schwanniomyces occidentalis
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C:Accession: S06115
R:Strasser, A.W.M.; Selk, R.; Dohmen, R.J.; Niermann, T.; Bielefeld, M.; Seeboth, P.; T.
Eur. J. Biochem. 184, 699-706, 1989
A:Title: Analysis of the alpha-amylase gene of Schwanniomyces occidentalis and the sec
A:Reference number: S06115; MUID:90032659; PMID:2806251
A:Accession: S06115
A:Molecule type: DNA
A:Residues: 1-512 <STR>
A:Cross-references: UNIPROT:P19269; EMBL:X16040; NID:g4882; PID:CAA334162.1; PID:g4883

C:Gene: AMY1

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-512/Product: alpha-amylase #status predicted <MAT>
F:209-336/Domain: alpha-amylase core homology <AMY>

Query Match 3.8%; Score 19; DB 2; Length 512;

Best Local Similarity 100.0%; Pred. No. 7.8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GIIDKLDYIQGMGFTAIWI 82
|||||
DB 80 GIIDKLDYIQGMGFTAIWI 98
|||||

RESULT 12
T38770
alpha-amylase a precursor - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38770
R:Skellton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z21751
A:Accession: T38770
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-513 <SK>
A:Cross-references: UNIPROT:O14154; EMBL:Z98762; PIDN:CAB11471.1; GSPDB:GN00066; SPDB:SE
A:Experimental source: strain 972h-; cosmid c4A8
C:Genetics:
A:Gene: SPDB:SPAC4A8.01
A:Map position: 1
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

Query Match 3.8%; Score 19; DB 2; Length 513;
Best Local Similarity 100.0%; Pred. No. 7.9e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GIIDKLDYIQGMGFTAIWI 82
|||||
DB 66 GIIDKLDYIQGMGFTAIWI 84
|||||

RESULT 13
JC4510
pullulanase (EC 3.2.1.41) precursor - yeast (Lipomyces kononenkoae)
N:Alternate names: LKA1 protein; raw starch-degrading amylase
N:Contains: alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)
C:Species: Lipomyces kononenkoae
C>Date: 07-Feb-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
C:Accession: JC4510; PC4116
R:Steyn, A.J.C.; Marmur, J.; Pretorius, I.S.
Gene 166, 65-71, 1995
A:Title: Cloning, sequence analysis and expression in yeasts of a cDNA containing a Lip
A:Reference number: JC4510; MUID:96105202; PMID:8529895
A:Molecule type: mRNA
A:Accession: JC4510
A:Residues: 1-624 <ST>
A:Cross-references: UNIPROT:Q01117; GB:U03076; NID:g1173536; PIDN:AAC49622.1; PID:g11735
A:Experimental source: strain IGC4052B
A:Accession: PC4116
A:Molecule type: protein
A:Residues: 29-44 <ST>
A:Experimental source: IGC4052B
C:Genetics:
A:Gene: LKA1
C:Function:
A:Description: hydrolyzes raw starch, degrading both alpha-1,4 and alpha-1,6 linkages
A:Pathway: glycogen/starch degradation
C:Superfamily: Lipomyces alpha-amylase; alpha-amylase core homology; glucoamylase starch
C:Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-624/Product: alpha-amylase #status predicted <MAT>
F:48-141/Domain: Glucoamylase starch-binding domain homology <SBD>
F:320-447/Domain: alpha-amylase core homology <AMY>
F:177-185,297-311,387-430,587-622/Disulfide bonds: #status predicted
F:304,344/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:357,377,444/Active site: His, Glu, Asp #status predicted

Query Match 3.2%; Score 16; DB 1; Length 624;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 NYSIDGLRIDTVKHVQ 232
|||||
DB 344 NYSIDGLRIDTVKHVQ 359
|||||

RESULT 14
A35282
alpha-amylase (EC 3.2.1.1) - Aspergillus niger
C:Species: Aspergillus niger
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A35282
R:Boel, E.; Brady, L.; Brzozowski, A.M.; Derewenda, Z.; Dodson, G.G.; Jensen, V.J.; Pete
Biochemistry 29, 6244-6249, 1990
A:Title: Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-angstrom
A:Reference number: A35282; MUID:91002514; PMID:2207069
A:Accession: A35282
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-484 <BO>
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:173-300/Domain: alpha-amylase core homology <AMY>

Query Match 2.8%; Score 14; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 9.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 LDYIQGMGFTAIWI 82
|||||
DB 49 LDYIQGMGFTAIWI 62
|||||

RESULT 15
S31478
alpha-amylase (EC 3.2.1.1) - Thermoactinomyces vulgaris
C:Species: Thermoactinomyces vulgaris
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S31478
R:Hofemeister, B.; Koenig, S.; Hoang, V.; Engel, J.; Mayer, G.; Heese, O.; Hansen, G.; H
submitted to the EMBL Data Library, December 1992
A:Description: The gene amyTV coding for a non-glucogenic alpha-amylase from Thermoactin
A:Reference number: S31478
A:Accession: S31478
A:Molecule type: DNA
A:Residues: 1-482 <HO>
A:Cross-references: UNIPROT:Q60051; EMBL:X69807; NID:g48289; PIDN:CAA49465.1; PID:g48290
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:194-319/Domain: alpha-amylase core homology <AMY>

Query Match 2.4%; Score 12; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 MGFTAIWITPVT 86
|||||
DB 89 MGFTAIWITPVT 100
|||||

Search completed: November 7, 2005, 19:33:47
Job time : 62.5676 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 19:00:20 ; Search time 264.382 Seconds
(without alignments)
964.571 Million cell updates/sec

Title: US-10-820-200-2
Perfect score: 498
Sequence: 1 MVAWWSFLYGLQVAAPALA.....LPRVLVPTPEKLAKSGKICSSS 498

Scoring table:
Oligo Gap 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_eprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	100.0	498	2 Q76CT3	Q76ct3 aspergillus
2	498	100.0	499	1 AMYA ASPOR	P10529 aspergillus
3	397	79.7	499	1 AMY ASPSH	P30292 aspergillus
4	397	79.7	499	2 Q76L99	Q76l99 aspergillus
5	384	77.1	498	1 AMYA ASPAW	Q02905 aspergillus
6	384	77.1	499	1 AMYB ASPAW	Q02906 aspergillus
7	342	68.7	499	2 Q96TH4	Q96th4 aspergillus
8	342	68.7	499	2 Q7LV45	Q7lv45 aspergillus
9	23	4.6	623	2 Q9UV09	Q9uv09 emericella
10	20	4.0	507	1 AMY2 DBEBC	Q08806 debaryomyce
11	19	3.8	490	2 Q9UV07	Q9uv07 emericella
12	19	3.8	512	1 AMY1 DBEBC	P19269 debaryomyce
13	19	3.8	513	1 AMY3 SCHPO	O14154 schizosacch
14	16	3.2	624	1 AMY1 LIPKO	Q01117 lipomyces k
15	16	3.2	647	2 Q6VF33	Q6vf33 lipomyces s
16	14	2.8	634	2 Q76L96	Q76l96 aspergillus
17	14	2.8	640	2 O13296	O13296 aspergillus
18	12	2.4	482	2 Q60051	Q60051 thermoactin
19	12	2.4	492	2 Q7SDJ6	Q7sdj6 neurospora
20	12	2.4	1196	1 AMYB PABPO	P21543 paenibacill
21	11	2.2	484	1 AMYA ASPNG	P56271 aspergillus
22	11	2.2	494	1 AMY1 SACFI	P21567 saccharomyc
23	10	2.0	128	2 O15751	O15751 dictyosteli
24	10	2.0	533	2 Q7S4K0	Q7s4k0 neurospora
25	10	2.0	625	2 Q74922	Q74922 schizosacch
26	10	2.0	631	2 Q92394	Q92394 cryptococcu
27	9	1.8	90	2 Q651X5	Q651x5 oryza sativ
28	9	1.8	199	2 Q7VXM8	Q7vxm8 bordetella
29	9	1.8	225	2 Q7WI40	Q7wi40 bordetella
30	9	1.8	229	2 Q7W674	Q7w674 bordetella
31	9	1.8	421	2 Q82BV7	Q82bv7 streptomyce

RESULT 1

ID	Q76CT3	PRELIMINARY;	PRT;	498 AA.
AC	Q76CT3;			
DT	05-JUL-2004 (Tremblrel. 27, Created)			
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	Alpha-amyase.			
GN	Name=amyA;			
OS	Aspergillus kawachi (Aspergillus awamori var. kawachi).			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;			
OC	Eurotiaceae; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.			
OX	NCBI_TaxID=40384;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Ito K.;			
RL	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.			
CC	-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.			
DR	EMBL; AB109452; BAD01051.1; -.			
DR	GO; GO:0004556; F:alpha-amyase activity; IEA.			
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro; IPR006047; Alpha amyl cat.			
DR	InterPro; IPR006589; Alp_aml cat sub.			
DR	InterPro; IPR006046; Glyco_hydro_13.			
DR	Pfam; PF00128; Alpha-amyase; 1.			
DR	PRINTS; PR00110; ALPHAAMYLASE.			
DR	SMART; SM00642; Aamy; 1.			
SQ	SEQUENCE 498 AA; 54679 MW; 8407BBFC7F4E3FC0 CRC64;			
Query Match	100.0%;	Score 498;	DB 2;	Length 498;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 498;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MVAVWSFLYGLQVAAPALAATPADWRSQSIYFLLTDFRFTDGTGTTATCNTADQKVC	60	
Db	1	MVAVWSFLYGLQVAAPALAATPADWRSQSIYFLLTDFRFTDGTGTTATCNTADQKVC	60	
QY	61	TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAVHYGWQDDIYSLNENYGTD	120	
Db	61	TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAVHYGWQDDIYSLNENYGTD	120	
QY	121	KALSSALLHERGMYLMVDVNVANMGVDGAGSSVDYVFRPFSSQDYFHPFCFTQNYED	180	
Db	121	KALSSALLHERGMYLMVDVNVANMGVDGAGSSVDYVFRPFSSQDYFHPFCFTQNYED	180	
QY	181	VEDCVLGNTVSLPDLTTDKVVKNEWYDVGSLVSNYSIDGLRIDTVKHVKDQDFWPG	240	
Db	181	VEDCVLGNTVSLPDLTTDKVVKNEWYDVGSLVSNYSIDGLRIDTVKHVKDQDFWPG	240	
QY	241	KAAGVYCGEVLGDGPAYTCPYQNVMDGVLYNPIYYPPLNAFKSTSGSMDLLYNMINT	300	
Db	241	KAAGVYCGEVLGDGPAYTCPYQNVMDGVLYNPIYYPPLNAFKSTSGSMDLLYNMINT	300	
QY	301	SDCPDSTLLGTFTVENHNDPRFASYNIDIALAKNVAFIINDGIPPIYAGQEQHAGGND	360	

ALIGNMENTS

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Db 301 SDCPDSTLLGTVEVNDHNPFRFASVTNDIALAKNVAFIILNDGIPILVAGQSQHVAGND 360
QY 361 PANREATWLSGYPTDSELYKLTASANAIRNYAISKDTGFTVTKNWPYKDDTTIAMRGT 420
Db 361 PANREATWLSGYPTDSELYKLTASANAIRNYAISKDTGFTVTKNWPYKDDTTIAMRGT 420
QY 421 DGSQVITVILSNKGAGSDSYTLISLSGAGYTAGOOLTEVIGCTTIVTSGDGNVPPVAGGLP 480
Db 421 DGSQVITVILSNKGAGSDSYTLISLSGAGYTAGOOLTEVIGCTTIVTSGDGNVPPVAGGLP 480
QY 481 RVLYPTEKLAGSKICSSS 498
Db 481 RVLYPTEKLAGSKICSSS 498

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RESULT 2

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ID AMYA ASPOR
AC P10529; P11763; Q00250; STANDARD; PRT; 499 AA.
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase A precursor (EC 3.2.1.1) (Taka-amylase A) (TAA) (1,4-
  alpha-D-glucan glucanohydrolase).
GN Name=AMY1;
GN and
GN Name=AMY2;
GN and
GN Name=AMY3;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutriales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 63303;
RX MEDLINE=89237897; PubMed=2785629;
RA Wirsal S., Lachmund A., Wildhardt G., Rutkowski E.;
RT "Three alpha-amylase genes of Aspergillus oryzae exhibit identical
  intron-exon organization.";
RL Mol. Microbiol. 3:3-14 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6;
RA Genes M.J., Dove M.J., Seligy V.L.; identical Taka-amylase genes, each
  containing eight introns.";
RL Gene 79:117-117(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Tada S., Iimura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.;
RT "Cloning and nucleotide sequence of the genomic Taka-amylase A gene of
  Aspergillus oryzae.";
RL Agric. Biol. Chem. 53:593-599 (1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=9012876; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
RA Tsukagoshi N., Furuoka M., Nagaba H., Kirita N., Tsuboi A., Udagaki S.;
RT "Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A:
  evidence for multiple related genes.";
RL Gene 84:319-327(1989).
RN [5]
RP SEQUENCE OF 22-499.
RA Toda H., Kondo K., Narita K.;
RT "The complete amino acid sequence of Taka-amylase A.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 58:208-212(1982).
RN [6]
RP SEQUENCE OF 206-225.
RX MEDLINE=74001521; PubMed=4733850;
RA Isemura S., Ikenaka T.;
RT "The amino acid sequences of glycopeptides obtained from Taka-amylase
  A with trypsin and chymotrypsin.";

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RL J. Biochem. 74:1-10 (1973).
RN [7]
RP SEQUENCE OF 433-499.
RA Narita K.;
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290 (1975).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=80227691; PubMed=6156152;
RA Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
  Toda H., Narita K., Kakudo M.;
RT "Molecular structure of taka-amylase A. I. Backbone chain folding at
  3-A resolution.";
RL J. Biochem. 87:1555-1558 (1980).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=84212370; PubMed=6609921;
RA Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
RT "Structure and possible catalytic residues of Taka-amylase A.";
RL J. Biochem. 95:697-702 (1984).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
RX MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
RA Brzowski A.M., Davies G.J.;
RT "Structure of the Aspergillus oryzae alpha-amylase complexed with the
  inhibitor acarbose at 2.0-A resolution.";
RL Biochemistry 36:10837-10845 (1997).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
  linkages in oligosaccharides and polysaccharides.
CC -!- COPACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
  at high concentrations.
CC -!- SUBUNIT: Monomer.
CC -!- BIOTECHNOLOGY: Used in the brewing industry to increase the
  fermentability of beer worts (including those made from unmalted
  cereals), in the starch industry to make high maltose and high DE
  syrups (starch saccharification), in the alcohol industry to
  reduce fermentation time, in the cereal food industry for flour
  supplementation and improvement of chilled and frozen dough, and
  in the forestry industry for low-temperature modification of
  starch. Sold under the name Fungamyl by Novozymes.
CC -!- MISCELLANEOUS: The sequence of AMY1 and AMY2 is shown.
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
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  or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X12725; CAA31218.1; -
CC EMBL; X12726; CAA31219.1; -
CC EMBL; X12727; CAA31220.1; -
CC EMBL; D00434; BAA00336.1; -
CC EMBL; M33218; AAA32708.1; -
CC PIR; JK0201; JK0201.
CC PIR; JT0466; JT0466.
CC PIR; S04548; ALAS1.
CC PDB; 2TAA; X-ray; A=22-499.
CC PDB; 6TAA; X-ray; @=22-499.
CC PDB; 7TAA; X-ray; @=22-499.
CC GlycoSuiteDB; P10529; -
CC InterPro; IPR006589; Alp_amy1_cat_sub.
CC InterPro; IPR006047; Alp_amy1_cat.
CC InterPro; IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; Alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAAMYLASE.
CC SMART; SM00642; Amyy; 1.
CC 3D-structure; Calcium-binding; Carbohydrate metabolism;
  Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
  Multigene family; Signal.
FT SIGNAL 1 21
FT CHAIN 22 499 Alpha-amylase A.

```


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CC EMBL; D10461; BAA01255.1; --
CC HSPF; F10529; 7TAA.
DR InterPro; IPR006589; Alp_aml_cat_sub.
DR InterPro; IPR006047; Alpha_aml_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
KW Hydroxylase; Signal.
FT SIGNAL 1 21
FT CHAIN 22 499
FT ACT_SITE 227 227 Alpha-amyase.
FT ACT_SITE 251 251 Nucleophile (By similarity).
FT ACT_SITE 318 318 Proton donor (By similarity).
FT METAL 142 142 By similarity.
FT METAL 183 183 Calcium 1 (By similarity).
FT METAL 196 196 Calcium 1 (via carbonyl oxygen) (By
FT METAL 227 227 similarity).
FT METAL 231 231 Calcium 2 (By similarity).
FT METAL 251 251 Calcium 2 (By similarity).
FT DISULFID 51 59 By similarity.
FT DISULFID 171 185 By similarity.
FT DISULFID 261 304 By similarity.
FT DISULFID 461 496 By similarity.
FT CARBOHYD 218 218 N-linked (GlcNAc...) (By similarity).
SQ SEQUENCE 499 AA; 54852 MW; 1PB7AE50DA01C03F CRC64;

Query Match 79.7%; Score 397; DB 1; Length 499;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCGG 60
DB 2 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCGG 61

QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAGHYGWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAGHYGWQDIYSLNENYGTADDL 121

QY 121 KALSSALHERGMVLDVVAHMGYDAGSSVDYSVFKPFSQDYFHPFCFIQNYEDQTO 180
DB 122 KALSSALHERGMVLDVVAHMGYDAGSSVDYSVFKPFSQDYFHPFCFIQNYEDQTO 181

QY 181 VEDCWLGDNTVSLPDLDTTKOVVKNWYDWGSLVSNYSIDGLRIDTVKHQKDFPWPYGN 240
DB 182 VEDCWLGDNTVSLPDLDTTKOVVKNWYDWGSLVSNYSIDGLRIDTVKHQKDFPWPYGN 241

QY 241 KAAGYVICGEVLGDGPAYTCYQNVMDGVNLNPIYYPILLNAPFKSTSGSMDDLNNINTVK 300
DB 242 KAAGYVICGEVLGDGPAYTCYQNVMDGVNLNPIYYPILLNAPFKSTSGSMDDLNNINTVK 301

QY 301 SDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAFIILNDGIPPIIYAGQEHYAGND 360
DB 302 SDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAFIILNDGIPPIIYAGQEHYAGND 361

QY 361 PANREATWLSGYPDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 420
DB 362 PANREATWLSGYPDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 421

QY 421 DGSQIVTILSNKGASGDSYTLISLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGIP 480
DB 422 DGSQIVTILSNKGASGDSYTLISLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGIP 481

QY 481 RVLYPTEKLAGSKICSSS 498
DB 482 RVLYPTEKLAGSKICSSS 499

RESULT 4
076L99 PRELIMINARY; PRT; 499 AA.
ID Q76L99
AC Q76L99;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amyase precursor.
GN Name=amyl 1;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT-11;
RA Matsubara T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB083159; BAD06002.1; -.
DR GO; GO:0004556; F:alpha-amyase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_aml_cat.
DR InterPro; IPR006589; Alp_aml_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL 1 21 Potential.
SQ SEQUENCE 499 AA; 54794 MW; 2B357AE38B36C1C2 CRC64;

Query Match 79.7%; Score 397; DB 2; Length 499;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCGG 60
DB 2 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCGG 61

QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAGHYGWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAGHYGWQDIYSLNENYGTADDL 121

QY 121 KALSSALHERGMVLDVVAHMGYDAGSSVDYSVFKPFSQDYFHPFCFIQNYEDQTO 180
DB 122 KALSSALHERGMVLDVVAHMGYDAGSSVDYSVFKPFSQDYFHPFCFIQNYEDQTO 181

QY 181 VEDCWLGDNTVSLPDLDTTKOVVKNWYDWGSLVSNYSIDGLRIDTVKHQKDFPWPYGN 240
DB 182 VEDCWLGDNTVSLPDLDTTKOVVKNWYDWGSLVSNYSIDGLRIDTVKHQKDFPWPYGN 241

QY 241 KAAGYVICGEVLGDGPAYTCYQNVMDGVNLNPIYYPILLNAPFKSTSGSMDDLNNINTVK 300
DB 242 KAAGYVICGEVLGDGPAYTCYQNVMDGVNLNPIYYPILLNAPFKSTSGSMDDLNNINTVK 301

QY 301 SDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAFIILNDGIPPIIYAGQEHYAGND 360
DB 302 SDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAFIILNDGIPPIIYAGQEHYAGND 361

QY 361 PANREATWLSGYPDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 420
DB 362 PANREATWLSGYPDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 421

QY 421 DGSQIVTILSNKGASGDSYTLISLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGIP 480
DB 422 DGSQIVTILSNKGASGDSYTLISLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGIP 481

QY 481 RVLYPTEKLAGSKICSSS 498
DB 482 RVLYPTEKLAGSKICSSS 499

```

RESULT 5
MYA ASPAW STANDARD; PRT; 498 AA.
ID AC Q02905;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amyase A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE Glucanohydrolase A).
GN Name=AMYA;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eukotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UVK143F;
RX MEDLINE=90254827; PubMed=2340591;
RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
RA Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
RT "Cloning, characterization, and expression of two alpha-amyase genes
RT from Aspergillus niger var. awamori.";
RL Curr. Genet. 17:203-212(1990).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X52755; CAA36966.1; -.
DR PIR; A48305; A48305.
DR HSSP; P10529; 7TAA.
DR InterPro; IPR006589; Alp_aml_cat_sub.
DR InterPro; IPR006047; Alpha_aml_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAAMYLAASE.
DR SMART; SM00642; Aamy; 1.
DR KEGG; 04512; Alpha-amyase; 1.
KW Hydrolyase; Multigene family; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 498 Alpha-amyase A.
FT ACT_SITE 227 227 Nucleophile (By similarity).
FT ACT_SITE 251 251 Proton donor (By similarity).
FT ACT_SITE 318 318 By similarity.
FT METAL 142 142 Calcium 1 (By similarity).
FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
FT similarity).
FT METAL 196 196 Calcium 1 (By similarity).
FT METAL 227 227 Calcium 2 (By similarity).
FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
FT similarity).
FT METAL 251 251 Calcium 2 (By similarity).
FT DISULFID 51 59 By similarity.
FT DISULFID 171 185 By similarity.
FT DISULFID 261 304 By similarity.
FT DISULFID 461 496 By similarity.
FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 498 AA; 54880 MW; 7658511BC01A8A01 CRC64;

Query Match 77.1%; Score 384; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6

MYB ASPAW

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ID AMYB ASPAW STANDARD; PRT; 499 AA.
AC Q02906;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amyase B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE Glucanohydrolase B).
GN Name=AMFB;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eukotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UVK143F;
RX MEDLINE=90254827; PubMed=2340591;
RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
RA Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
RT "Cloning, characterization, and expression of two alpha-amyase genes
RT from Aspergillus niger var. awamori.";
RL Curr. Genet. 17:203-212(1990).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X52756; CAA36967.1; -.
DR PIR; B48305; B48305.
DR HSSP; P10529; 7TAA.
DR InterPro; IPR006589; Alp_aml_cat_sub.
DR InterPro; IPR006047; Alpha_aml_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amyase; 1.

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DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
KW Hydrolase; Multigene family; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 499 Alpha-amylase B.
FT ACT_SITE 227 227 Nucleophile (By similarity).
FT ACT_SITE 251 251 Proton donor (By similarity).
FT ACT_SITE 318 318 By similarity.
FT METAL 142 142 Calcium 1 (By similarity).
FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By similarity).
FT METAL 196 196 Calcium 1 (By similarity).
FT METAL 227 227 Calcium 2 (By similarity).
FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By similarity).
FT METAL 251 251 Calcium 2 (By similarity).
FT DISULFID 51 59 By similarity.
FT DISULFID 171 185 By similarity.
FT DISULFID 261 304 By similarity.
FT DISULFID 461 496 By similarity.
FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 499 AA; 54921 MW; 740B9681BC01A8A CRC64;

Query Match 77.1%; Score 384; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAPADWRSQSIFLLTDRFARTDGTTCNTADQKCGG 60
DB 2 MVAMWSFLYGLQVAAPALAAPADWRSQSIFLLTDRFARTDGTTCNTADQKCGG 61

QY 61 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHGYWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHGYWQDIYSLNENYGTADDL 121

QY 121 KALSALHERGMYLMVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHFPCFIONYEDOTQ 180
DB 122 KALSALHERGMYLMVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHFPCFIONYEDOTQ 181

QY 181 VEDCWLGONTVSLPDLDTTKDVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240
DB 182 VEDCWLGONTVSLPDLDTTKDVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 241

QY 241 KAAGVYCI GEVLGDGPAYTCPYQNVMDGVNLNPIYYPILLNAPFKSTSGSMDDLNNMTVK 300
DB 242 KAAGVYCI GEVLGDGPAYTCPYQNVMDGVNLNPIYYPILLNAPFKSTSGSMDDLNNMTVK 301

QY 301 SDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPPIYAGQEOHYAGGND 360
DB 302 SDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPPIYAGQEOHYAGGND 361

QY 361 PANREATWLSGYPTDSELYKLIAS 384
DB 362 PANREATWLSGYPTDSELYKLIAS 385
```

RESULT 7

Q96TH4 ID Q96TH4 PRELIMINARY; PRT; 499 AA.

AC Q96TH4; PRELIMINARY; PRT; 499 AA.

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Taka-amylase A (EC 3.2.1.1).

GN Name=amyA;

OS Aspergillus oryzae.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

OX NCBI_TaxID=5062;

RN [1]_TaxID=5062;

RP SEQUENCE FROM N.A.

RC STRAIN=R1B40;

```
RX MEDLINE=20289310; PubMed=10830498;
RA Goni K., Akano T., Minetoki T., Ozeki K., Kumagai C., Okazaki N.,
RA Iimura Y.;
RT "Molecular cloning and characterization of a transcriptional activator
RT gene, amyR, involved in the amylolytic gene expression in Aspergillus
RT oryzae.";
RL Biosci. Biotechnol. Biochem. 64:816-827(2000).
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB021876; BAA95703.1; -.
DR PIR; JN0588; JN0588.
DR PIR; S04549; ALAS3.
DR HSSP; P10529; 7TAA.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0016738; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; Alpha-amylase; 1_13.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; EBF42ADA71D20DA9 CRC64;

Query Match 68.7%; Score 342; DB 2; Length 499;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 442; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 56 KYCGTGWGIIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHGYWQDIYSLNENY 115
DB 57 KYCGTGWGIIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHGYWQDIYSLNENY 116

QY 116 TADDLKALSSALHERGMYLMVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHFPCFIONY 175
DB 117 TADDLKALSSALHERGMYLMVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHFPCFIONY 176

QY 176 EDQTVQEDCWLGONTVSLPDLDTTKDVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDF 235
DB 177 EDQTVQEDCWLGONTVSLPDLDTTKDVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDF 236

QY 236 WPGYNKAAGVYCI GEVLGDGPAYTCPYQNVMDGVNLNPIYYPILLNAPFKSTSGSMDDLNNM 295
DB 237 WPGYNKAAGVYCI GEVLGDGPAYTCPYQNVMDGVNLNPIYYPILLNAPFKSTSGSMDDLNNM 296

QY 296 INTVKSDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPPIYAGQEOHY 355
DB 297 INTVKSDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPPIYAGQEOHY 356

QY 356 AGGNDPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFTYKKNWPIYKDDTTIA 415
DB 357 AGGNDPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFTYKKNWPIYKDDTTIA 416

QY 416 MRKGTGDSQIVTILSNKGASGDSYTLISGAGYTAGQOLTVEIGCTTVTSGDGNVPVPM 475
DB 417 MRKGTGDSQIVTILSNKGASGDSYTLISGAGYTAGQOLTVEIGCTTVTSGDGNVPVPM 476

QY 476 AGGLPRVLYPTEKLAGSKICSSS 498
DB 477 AGGLPRVLYPTEKLAGSKICSSS 499
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RESULT 8

Q7LV45 ID Q7LV45 PRELIMINARY; PRT; 499 AA.

AC Q7LV45; PRELIMINARY; PRT; 499 AA.

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Alpha-amylase (EC 3.2.1.1).

GN Name=amy1; flavus.

OS Aspergillus

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

```
OX NCBI_TaxID=5059;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=86-10D;
RA Fakhoury A.M., Woloshuk C.P.;
RT "Amy1, the alpha-amylase gene of Aspergillus flavus: Involvement in
RT aflatoxin biosynthesis in maize kernels.";
RL Phytopathology 89:908-914(1999).
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AF139925; AAF14264.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Aamy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;

Query Match 68.7%; Score 342; DB 2; Length 499;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 442; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 56 KYCGGTWQGIIDKLDYIQMGFTAIWITPTAQLPQTAYGDAYHYGYWQDIYSLNENYG 115
DB 57 KYCGGTWQGIIDKLDYIQMGFTAIWITPTAQLPQTAYGDAYHYGYWQDIYSLNENYG 116

QY 116 TADDLKALSSALHERGMVLMVDVANHMGYDYGAGSSVDYVFKPFSSQDYFHPFCFIQNY 175
DB 117 TADDLKALSSALHERGMVLMVDVANHMGYDYGAGSSVDYVFKPFSSQDYFHPFCFIQNY 176

QY 176 EDQTOVEDCWLGDNTVSLPDLTTKDVKNKNEWDMVGLSVSNYSIDGLRIDTVKHKQDF 235
DB 177 EDQTOVEDCWLGDNTVSLPDLTTKDVKNKNEWDMVGLSVSNYSIDGLRIDTVKHKQDF 236

QY 236 WFGYNKAAGVYCIQGVLDGDPATYTCYQNVMDGLNYPYIPLLNAPKSTSGSMDLYNM 295
DB 237 WFGYNKAAGVYCIQGVLDGDPATYTCYQNVMDGLNYPYIPLLNAPKSTSGSMDLYNM 296

QY 296 INTVKSDCPSDSTLLGTFVENHNDNPFASVTNDIALAKNVAFTIINDGIPPIYAGQEQHY 355
DB 297 INTVKSDCPSDSTLLGTFVENHNDNPFASVTNDIALAKNVAFTIINDGIPPIYAGQEQHY 356

QY 356 AGGNPDANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTYKNWPIYKDDTTIA 415
DB 357 AGGNPDANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTYKNWPIYKDDTTIA 416

QY 416 MRKGTGDSQIVTILSNKAGSDSYTILSLGAGYTAGQQLTETVIGCTTIVTSGDGNVPVPM 475
DB 417 MRKGTGDSQIVTILSNKAGSDSYTILSLGAGYTAGQQLTETVIGCTTIVTSGDGNVPVPM 476

QY 476 AGGLPRVLYPTEKLAGSKICSSS 498
DB 477 AGGLPRVLYPTEKLAGSKICSSS 499

RESULT 9
Q9UV09 PRELIMINARY; PRT; 623 AA.
AC Q9UV09;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN Name=amyB;
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
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RP SEQUENCE FROM N.A.
RA Boase N.A., Murphy R.L., Kelly J.M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AF208224; AAF17100.1; -.
DR HSP; P56271; 2AAA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_l3.
DR InterPro; IPR002044; Glyco_hydro_CBD.
DR Pfam; PF00128; Alpha-amylase; 1.
DR Pfam; PF00686; CBM 20; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR ProDom; PD001568; Glyco_hydro_CBD; 1.
DR SMART; SM00642; Aamy; 1.
SQ SEQUENCE 623 AA; 68598 MW; 822F002C37F5A9A4 CRC64;

Query Match 4.6%; Score 23; DB 2; Length 623;
Best Local Similarity 100.0%; Pred. No. 2.2e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 WRSQSIYELLTDREFARTDGTSTA 48
DB 25 WRSQSIYELLTDREFARTDGTSTA 47

RESULT 10
AMY2 DEBOC
ID AMY2 DEBOC STANDARD; PRT; 507 AA.
AC Q08806;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase 2 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase 2).
GN Name=SWA2;
OS Debaryomyces occidentalis (Yeast) (Schwanniomyces occidentalis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=27300;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 26077 / CBS 2863;
RX MEDLINE=93365041; PubMed=8358835;
RA Claros M.G., Abarca D., Fernandez-Lobato M., Jimenez A.;
RT "Molecular structure of the SWA2 gene encoding an AMY1-related alpha-
RT amylase from Schwanniomyces occidentalis.";
RL Curr. Genet. 24:75-83(1993).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X73497; CAA51912.1; -.
CC PIR; S33921; S33921.
CC HSP; P10529; 7TAA.
CC InterPro; IPR006589; Alp_amyl_cat_sub.
CC InterPro; IPR006047; Alpha_amyl_cat.
CC InterPro; IPR006046; Glyco_hydro_l3.
CC Pfam; PF00128; Alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAAMYLASE.
```

DR SMART; SM00642; Aamy; 1.
 KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 FT SIGNAL 1 20 Potential.
 FT CHAIN 21 507 Alpha-amyase 2.
 FT ACT_SITE 238 238 Nucleophile (By similarity).
 FT ACT_SITE 262 262 Proton donor (By similarity).
 FT ACT_SITE 329 329 By similarity.
 FT METAL 153 153 Calcium 1 (By similarity).
 FT METAL 194 194 Calcium 1 (via carbonyl oxygen) (By similarity).
 FT METAL 207 207 Calcium 1 (By similarity).
 FT METAL 238 238 Calcium 2 (By similarity).
 FT METAL 242 242 Calcium 1 (via carbonyl oxygen) (By similarity).
 FT METAL 262 262 Calcium 2 (By similarity).
 FT DISULFID 62 70 By similarity.
 FT DISULFID 182 196 By similarity.
 FT DISULFID 272 315 By similarity.
 FT DISULFID 470 505 By similarity.
 FT CARBOHYD 229 229 N-linked (GlcNAc...) (Probable).
 SQ SEQUENCE 507 AA; 55966 MW; 3A562B95BD8AD63 CRC64;

Query Match 4.0%; Score 20; DB 1; Length 507;
 Best Local Similarity 100.0%; Pred. No. 1.7e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 QGIIDKLDYIQMGFTAIWI 82
 |||||

Db 75 QGIIDKLDYIQMGFTAIWI 94
 |||||

RESULT 11

QYU0V07 PRELIMINARY; PRT; 490 AA.
 AC QYU0V07;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alpha-amyase AmyA.
 GN Name=amyA;
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eutiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=162425;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Boase N.A., Murphy R.M., Kelly J.M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 DR EMBL; AF208225; AAF17103.1; -;
 DR HSSP; P10329; 7TAA.
 DR GO; GO:0004556; F:alpha-amyase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006589; Alpha_aml cat.
 DR InterPro; IPR006589; Alp_aml cat sub.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amyase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Aamy; 1.
 SQ SEQUENCE 490 AA; 54249 MW; A891C4ACEABE5305 CRC64;

Query Match 3.8%; Score 19; DB 2; Length 490;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 LDYIQMGFTAIWIPTVTA 87
 |||||

Db 63 LDYIQMGFTAIWIPTVTA 81
 |||||

RESULT 12

AMY1_DEBOC

ID AMY1_DEBOC STANDARD; PRT; 512 AA.
 AC P19269;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DE Alpha-amyase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase 1).
 GN Name=AMY1.
 OS Debaryomyces occidentalis (Yeast) (Schwanniomyces occidentalis).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
 OX NCBI_TaxID=27300;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 26076;
 RX MEDLINE=90032659; PubMed=2806251;
 RA Strasser A.W.M., Selk R., Dohmen R.J., Niermann T., Bielefeld M.,
 RA Seeboth P., Tu G., Hollenberg C.P.;
 RT "Analysis of the alpha-amyase gene of Schwanniomyces occidentalis and
 the secretion of its gene product in transformants of different yeast
 genera.";
 RT Eur. J. Biochem. 184:699-706(1989).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CCRC 21164;
 RX MEDLINE=92120467; PubMed=1769525; DOI=10.1016/0378-1097(91)90280-N;
 RA Wu F.M., Wang T.T., Hsu W.H.;
 RT "The nucleotide sequence of Schwanniomyces occidentalis alpha-amyase
 gene.";
 RT FEMS Microbiol. Lett. 66:313-318(1991).
 RL [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=ATCC 26077 / CBS 2863;
 RX MEDLINE=92307400; PubMed=1612414;
 RA Park J.C., Bai S., Tai C.Y., Chun S.B.;
 RT "Nucleotide sequence of the extracellular alpha-amyase gene in the
 yeast Schwanniomyces occidentalis ATCC 26077.";
 RL FEMS Microbiol. Lett. 72:17-23(1992).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 linkages in oligosaccharides and polysaccharides.
 CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 at high concentrations (By similarity).
 CC -!- ENZYME REGULATION: Alpha-amyase expression underlies catabolite
 repression by glucose.
 CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC
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 CC
 DR EMBL; S7586; AAB21151.2; -;
 DR EMBL; X16040; CAA34162.1; -;
 DR EMBL; X62079; CAA43995.1; -;
 DR EMBL; S38381; AAB22383.2; -;
 DR PIR; S06115; S06115.
 DR PIR; S23355; S23355.
 DR HSSP; P10529; 7TAA.
 DR InterPro; IPR006589; Alp_aml cat sub.
 DR InterPro; IPR006047; Alpha_aml cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amyase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Aamy; 1.
 KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 KW Hydrolase; Signal.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 512 Alpha-amyase 1.
 FT ACT_SITE 242 242 Nucleophile (By similarity).
 FT ACT_SITE 266 266 Proton donor (By similarity).
 FT

```

FT ACT_SITE 333 333 By similarity.
FT METAL 157 157 Calcium 1 (By similarity).
FT METAL 198 198 Calcium 1 (via carbonyl oxygen) (By
FT METAL 211 211 similarity).
FT METAL 242 242 Calcium 1 (By similarity).
FT METAL 246 246 Calcium 2 (By similarity).
FT METAL 266 266 Calcium 1 (via carbonyl oxygen) (By
FT METAL 233 233 similarity).
FT CARBOHYD 233 233 Calcium 2 (By similarity).
FT DISULFID 66 74 N-linked (GlcNAc... ) (Probable).
FT DISULFID 196 200 By similarity.
FT DISULFID 276 319 By similarity.
FT DISULFID 475 510 By similarity.
FT VARIANT 32 32 M -> K (in strain CCRC 21164 and strain
FT VARIANT 36 36 ATCC 26077).
FT VARIANT 73 73 S -> G (in strain CCRC 21164).
FT VARIANT 280 280 Y -> I (in strain ATCC 26077).
FT VARIANT 350 350 N -> S (in strain CCRC 21164).
FT VARIANT 479 479 D -> A (in strain CCRC 21164 and strain
FT VARIANT 483 483 ATCC 26077).
FT VARIANT 512 479 L -> S (in strain CCRC 21164 and strain
FT VARIANT 483 483 ATCC 26077).
FT SEQUENCE 512 AA; 56527 MW; 857552B2CF60F965 CRC64;
SQ SEQUENCE 512 AA; 56527 MW; 857552B2CF60F965 CRC64;

Query Match 3.8%; Score 19; DB 1; Length 512;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GIIDKLDYIQGMGFTAIWI 82
DB 80 GIIDKLDYIQGMGFTAIWI 98

RESULT 13
AMY3 SCHPO STANDARD; PRT; 513 AA.
AC O14154; Q874R5; Q96WR6;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 36, Last annotation update)
DE Probable alpha-amylase meu30 precursor (BC 3.2.1.1) (1,4-alpha-D-
DE glucan glucanohydrolase) (Meiotic expression up-regulated protein 30).
OS Name=me5; Synonymys=meu30; ORFNames=SPAC25H1.09, SPAC4A8.01;
GN Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21048401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Guilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Murgall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch B.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds R., Squares R., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer C., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leinhardt R., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaou E., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

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RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McComb W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:1871-880(2002).
RN [2]
RP SEQUENCE OF 191-513 FROM N.A.
RC STRAIN=CD16-1;
RX MEDLINE=21270454; PubMed=11376151; DOI=10.1093/nar/29.11.2327;
RA Watanabe T., Miyashita K., Saito T.T., Yoneki T., Kakiyama Y.,
RA Nabeshima K., Kishi Y.A., Shimoda C., Nojima H.;
RT "Comprehensive isolation of meiosis-specific genes identifies novel
RT proteins and unusual non-coding transcripts in Schizosaccharomyces
RT pombe.";
RL Nucleic Acids Res. 29:2327-2337(2001).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC
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CC
DR EMBL; Z98762; CAB11471.1; -.
DR EMBL; Z98944; CAD62442.1; -.
DR EMBL; AB054314; BAB60880.1; -.
DR PIR; T38770; T38770.
DR HSP; P10529; 7TAA.
DR GenedB SPombe; SPAC25H1.09; -.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; Alpha-amylase; 1.
DR SMART; SM00642; Aamy; 1.
KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
KW Hydrolyase; Meiosis; Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 513 Probable alpha-amylase meu30.
FT ACT_SITE 226 226 Nucleophile (By similarity).
FT ACT_SITE 250 250 Proton donor (By similarity).
FT ACT_SITE 318 318 By similarity.
FT METAL 143 143 Calcium 1 (By similarity).
FT METAL 182 182 Calcium 1 (via carbonyl oxygen) (By
FT METAL 195 195 similarity).
FT METAL 226 226 Calcium 1 (By similarity).
FT METAL 230 230 Calcium 2 (By similarity).
FT METAL 250 250 Calcium 1 (via carbonyl oxygen) (By
FT DISULFID 52 60 similarity).
FT DISULFID 171 184 Calcium 2 (By similarity).
FT DISULFID 260 304 By similarity.
FT DISULFID 454 488 By similarity.
FT CARBOHYD 162 162 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 357 357 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 513 AA; 58715 MW; 455DD97FA428C182 CRC64;

Query Match 3.8%; Score 19; DB 1; Length 513;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GIIDKLDYIQGMGFTAIWI 82
DB 66 GIIDKLDYIQGMGFTAIWI 84

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RESULT 14
AMYL_LIPKO
ID AMYL_LIPKO STANDARD; PRT; 624 AA.
AC Q01117;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase 1).
GN Name=LKAl;
OS Lipomyces kononenkoae.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Lipomycetaceae; Lipomyces.
OX NCBI_TaxID=34357;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IGC4052B;
RX MEDLINE=96132108; PubMed=8529895; DOI=10.1016/0378-1119(95)00633-0;
RA Steyn A.J.C., Marmur J., Pretorius I.S.;
RT "Cloning, sequence analysis and expression in yeasts of a cDNA
RT containing a Lipomyces kononenkoae alpha-amylase-encoding gene.";
RL Gene 166:65-71(1995).
RN [2]
RP SEQUENCE OF 29-44.
RC STRAIN=IGC4052B;
RX MEDLINE=96132108; PubMed=8593683;
RA Steyn A.J.C., Pretorius I.S.;
RT "Characterization of a novel alpha-amylase from Lipomyces kononenkoae
RT and expression of its gene (LKAl) in Saccharomyces cerevisiae.";
RL Curr. Genet. 28:526-533(1995).
CC -! CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -! COPACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -! SUBCELLULAR LOCATION: Secreted.
CC -! SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -! SIMILARITY: Contains 1 carbohydrate binding type-21 (CBM21)
CC domain.
-----
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-----
DR EMBL; U30376; AAC49622.1; ALT_INIT.
DR FIR; JC4510; JC4510.
DR HSSP; P10529; 7TAA.
DR InterPro; IPR006589; Alp amyl cat sub.
DR InterPro; IPR006047; Alpha amyl_cat.
DR InterPro; IPR005036; CBM 21.
DR Pfam; PF00128; Alpha-amylase; 1.
DR Pfam; PF03370; CBM_21; 1.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00642; Amy; 1.
KW Glycoprotein; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 28
FT CHAIN 29 624 Alpha-amylase 1.
FT DOMAIN 40 133 Carbohydrate binding type-21.
FT ACT_SITE 353 353 Nucleophile (By similarity).
FT ACT_SITE 377 377 Proton donor (By similarity).
FT ACT_SITE 444 444 By similarity.
FT METAL 268 268 Calcium 1 (By similarity).
FT METAL 309 309 Calcium 1 (via carbonyl oxygen) (By
FT similarity).
FT METAL 322 322 Calcium 1 (By similarity).
FT METAL 353 353 Calcium 2 (By similarity).
FT METAL 357 357 Calcium 1 (via carbonyl oxygen) (By
FT similarity).
FT METAL 377 377 Calcium 2 (By similarity).
FT DISULFID 177 185 By similarity.
```

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FT DISULFID 297 311 By similarity.
FT DISULFID 387 430 By similarity.
FT DISULFID 587 622 By similarity.
FT CARBOHYD 304 304 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 344 344 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 624 AA; 68876 MW; 87EB16534F5A9A9F CRC64;

Query Match 3.2%; Score 16; DB 1; Length 624;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 217 NYSIDGLRIDTVKHVQ 232
Db 344 NYSIDGLRIDTVKHVQ 359

RESULT 15
Q6YF33
ID Q6YF33 PRELIMINARY; PRT; 647 AA.
AC Q6YF33;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase.
OS Lipomyces starkeyi.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Lipomycetaceae; Lipomyces.
OX NCBI_TaxID=29829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM 22M;
RX PubMed=15043869; DOI=10.1016/j.femsle.2004.01.036;
RA Kang H.K., Lee J.H., Kim D., Day D.F., Robyt J.F., Park K.-H.,
RA Moon T.-W.;
RT "Cloning and expression of Lipomyces starkeyi alpha-amylase in
RT Escherichia coli and determination of some of its properties.";
RL FEMS Microbiol. Lett. 233:53-64(2004).
DR EMBL; AY155463; AAN75021.1; -.
DR HSSP; P26827; 1A47.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl_cat.
DR InterPro; IPR006589; Alp amyl_cat_sub.
DR InterPro; IPR005036; CBM 21.
DR Pfam; PF00128; Alpha-amylase; 1.
DR Pfam; PF03370; CBM_21; 1.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 647 AA; 70957 MW; D946071DB7560144 CRC64;

Query Match 3.2%; Score 16; DB 2; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 217 NYSIDGLRIDTVKHVQ 232
Db 367 NYSIDGLRIDTVKHVQ 382

Search completed: November 7, 2005, 19:32:38
Job time : 266.382 secs
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:58:55 ; Search time 286.494 Seconds
(without alignments)
672.288 Million cell updates/sec

Title: US-10-820-200-2
Perfect score: 498
Sequence: 1 MVAWWSFLYGLQVAPALAA.....LPRVLVPTKLAGSKICSSS 498

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : A_Geneseq_16Dec04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	100.0	498	AAB84206	Aab84206 Amino aci
2	391	78.5	478	AAR72450	Aar72450 Aspergill
3	391	78.5	478	AAR78270	Aar78270 Aspergill
4	391	78.5	478	AAW14500	Aaw14500 Aspergill
5	384	77.1	498	ADT89632	Adt89632 Aspergill
6	384	77.1	499	ADT89628	Adt89628 Aspergill
7	377	75.7	1095	ABP96630	Abp96630 Alpha-amy
8	238	47.8	478	AAR79025	Aar79025 Mature ta
9	226	45.4	478	AAR46065	Aar46065 Mutant al
10	73	14.7	423	ABBO9072	Abbo9072 Aspergill
11	45	9.0	46	AAP70311	Aap70311 Sequence
12	45	9.0	46	AAP94631	Aap94631 Aspergill
13	45	9.0	46	AAR24437	Aar24437 Sequence
14	23	4.6	495	ABB80177	Abb80177 A. fumiga
15	20	4.0	20	ADP19639	Adp19639 Aspergill
16	20	4.0	21	ADM36200	Adm36200 Alpha-amy
17	20	4.0	21	ADO27369	Ado27369 A. niger
18	20	4.0	494	ABP97894	Abp97894 Amino aci
19	19	3.8	511	AAP81161	Aap81161 Recombina
20	19	3.8	511	AAPE81180	Aape81180 Sequence
21	19	3.8	512	AAR07574	Aar07574 Alpha-amy
22	19	3.8	513	ADM19570	Adm19570 Bacterial
23	18	3.6	46	AAP95651	Aap95651 N-termina
24	18	3.6	52	ADC22919	Adc22919 Conserved
25	18	3.6	54	AAP94633	Aap94633 N-termina

26	18	3.6	304	2	AAW44272	Aaw44272 Hybrid DN
27	18	3.6	306	2	AAW44269	Aaw44269 Hybrid DN
28	18	3.6	306	2	AAW44270	Aaw44270 Hybrid DN
29	18	3.6	307	2	AAW44273	Aaw44273 Hybrid DN
30	18	3.6	308	2	AAW44271	Aaw44271 Hybrid DN
31	18	3.6	630	6	ABB80178	Abb80178 A. fumiga
32	14	2.8	55	2	AAR88213	Aar88213 Alpha-amy
33	14	2.8	493	2	AAR88212	Aar88212 Alpha-amy
34	13	2.6	13	3	AAB12599	Aab12599 Amino aci
35	13	2.6	567	6	ABP97899	Abp97899 Amino aci
36	12	2.4	500	8	ADS23436	Ads23436 Bacterial
37	12	2.4	547	6	ABB80179	Abb80179 A. fumiga
38	12	2.4	549	6	ABP97895	Abp97895 Amino aci
39	12	2.4	555	6	ABP97896	Abp97896 Amino aci
40	11	2.2	49	1	AAP94634	Aap94634 N-termina
41	11	2.2	452	2	AAR63186	Aar63186 Variant a
42	11	2.2	468	2	AAR24136	Aar24136 Alpha-amy
43	11	2.2	468	2	AAR63184	Aar63184 Variant a
44	11	2.2	468	2	AAR63185	Aar63185 Variant a
45	11	2.2	468	2	AAR63187	Aar63187 Variant a

ALIGNMENTS

RESULT 1
AAB84206
ID AAB84206 standard; protein; 498 AA.
XX
AC AAB84206;
XX
DT 06-AUG-2001 (first entry)
XX
DE Amino acid sequence of a fungamyl-like alpha-amylase.
XX
KW Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose;
KW alcohol; starch; dough improver; brewing; starch liquification.
XX
OS Aspergillus oryzae.
XX
PN WO200134784-A1.
XX
PD 17-MAY-2001.
XX
PF 10-NOV-2000; 2000WO-DK000626.
XX
PR 10-NOV-1999; 99DK-00001617.
XX
PA (NOVO) NOVOZYMES AS.
XX
PI Bisgard-Frantzen H, Svendsen A, Pedersen S;
DR WPI; 2001-367478/38.
XX
N-PSDB; AAP90208.
XX
PT New variant of Fungamyl-like alpha-amylase, useful for production of
PT maltose syrups, includes mutations that improve stability against heat
PT and acidic pH.
XX
PS Claim 1; Page 42-45; 49pp; English.
XX
CC The present sequence represents a fungamyl-like alpha-amylase. The
CC specification describes variants of this fungamyl-like alpha-amylase,
CC which have an alteration in one the amino acid regions 98-110, 150-160,
CC 161-167, 280-288, 448-455, and 468-475. Each alteration is a deletion or
CC substitution of an amino acid or an insertion of an amino acid downstream
CC of a particular position. The variants retain alpha-amylase activity, and
CC have better heat stability and/or stability at acidic pH, relative to
CC wild-type enzyme. The variants can therefore be used at higher
CC temperatures (more efficient conversion or faster reaction, and have
CC reduced need for cooling and reduced risk of contamination). The variants
CC may also be used in conjunction with other enzymes, particularly
CC glucoamylase during dextrinisation. The variants are used to produce

CC syrups, particularly of high maltose content, or alcohol, from starch; as
CC dough improver for baked goods; in brewing, to increase fermentability of
CC the wort; and for liquefaction of starch

XX Sequence 498 AA;

Query Match 100.0%; Score 498; DB 4; Length 498;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVANWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGTTCNTADQKYGCG 60
DB 1 MVANWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGTTCNTADQKYGCG 60
QY 61 TWQGIIDKLDYIQGSGFTAIWITPVTQALPQTAYGDVHGYYWQDIYSLNENYGTADDL 120
DB 61 TWQGIIDKLDYIQGSGFTAIWITPVTQALPQTAYGDVHGYYWQDIYSLNENYGTADDL 120
QY 121 KALSSALHERGMYLMDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
DB 121 KALSSALHERGMYLMDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
QY 181 VEDCWLGNTVSLPDLDTTKVKNNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240
DB 181 VEDCWLGNTVSLPDLDTTKVKNNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240
QY 241 KAAGVYCIGEVLDGDPAYTCPYQNVMDGLNYPYIYPLLNAFKSTSGSMDDLNNMINTVK 300
DB 241 KAAGVYCIGEVLDGDPAYTCPYQNVMDGLNYPYIYPLLNAFKSTSGSMDDLNNMINTVK 300
QY 301 SDPCDSTLLGTVEVNDHNPREFASYTNDIALAKNVAAFIILNDGIPYIYAGQEHVAGGND 360
DB 301 SDPCDSTLLGTVEVNDHNPREFASYTNDIALAKNVAAFIILNDGIPYIYAGQEHVAGGND 360
QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 420
DB 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 420
QY 421 DGSQIVTILSNKGASDSTLSGAGYTAGOQLTEVIGCTVTVGSDGNVPVPMAGGLP 480
DB 421 DGSQIVTILSNKGASDSTLSGAGYTAGOQLTEVIGCTVTVGSDGNVPVPMAGGLP 480
QY 481 RVLYPTEKLAGSKICSSS 498
DB 481 RVLYPTEKLAGSKICSSS 498

RESULT 2

AAR72450
ID AAR72450 standard; protein; 478 AA.

XX AAR72450;

XX 25-MAR-2003 (revised)

DT 01-DEC-1995 (first entry)

XX Aspergillus oryzae alpha amylase (mature protein).

XX Alpha amylase; variant; enzyme; detergent; additive; dishwashing;
KW washing; Bacillus licheniformis; Bacillus amyloliquefaciens;
KW Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
KW thermostable.

OS Aspergillus oryzae.

XX WO9510603-A1.

XX 20-APR-1995.

XX 05-OCT-1994; 94WO-DK000370.

XX 08-OCT-1993; 93DK-00001133.

PR 02-FEB-1994; 94DK-00000140.

XX (NOVO) NOVO-NORDISK AS.

XX Borchert TV, Bisgard-Prantzen H, Svendsen A, Thellersen M;
PI Van Der Zee P;

XX WPI; 1995-161790/21.

XX New Bacillus derived alpha-amylase variants - having amino acid
PI modifications to improve washing and/or dishwashing performance.

XX Disclosure; Page 75-76; 105pp; English.

CC Variant alpha amylase enzymes which have improved washing and/or as
CC detergent additives. The enzymes have one or more amino acid residues
CC added, deleted or substituted. The variants can also be used for textile
CC desizing prior to scouring, bleaching and dyeing. The variants have
CC improved thermostability, acid/alkaline stability; low temperature
CC optimum; pH optimum; higher hydrolysis velocity and improved tolerance to
CC other composition constituents, e.g. oxidation agents. (Updated on 25-MAR
CC -2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 478 AA;

Query Match 78.5%; Score 391; DB 2; Length 478;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRPARTDGTTCNTADQKYGCGTWQGIIDKLDYIQGSGFTAI 80

DB 1 ATPADWRSQSIYFLLTDRPARTDGTTCNTADQKYGCGTWQGIIDKLDYIQGSGFTAI 60

QY 81 WITPVTQALPQTAYGDVHGYYWQDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140

DB 61 WITPVTQALPQTAYGDVHGYYWQDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120

QY 141 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTOVEDCWLGNTVSLPDLDTTK 200

DB 121 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTOVEDCWLGNTVSLPDLDTTK 180

QY 201 DVKNKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 260

DB 181 DVKNKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 240

QY 261 PYQNVMDGLNYPYIYPLLNAFKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDNPR 320

DB 241 PYQNVMDGLNYPYIYPLLNAFKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDNPR 300

QY 321 FASYTNDIALAKNVAAFIILNDGIPYIYAGQEHVAGGNDPANREATWLSGYPTDSELYK 380

DB 301 FASYTNDIALAKNVAAFIILNDGIPYIYAGQEHVAGGNDPANREATWLSGYPTDSELYK 360

QY 381 LIASANAIRNVAISKDTGFTVYKNWPIYKDD 411

DB 361 LIASANAIRNVAISKDTGFTVYKNWPIYKDD 391

RESULT 3

AAR78270

ID AAR78270 standard; protein; 478 AA.

XX AAR78270;

DT 17-JAN-1996 (first entry)

XX Aspergillus oryzae alpha amylase (mature protein).

XX Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch;
KW thermostable; methionine; Bacillus licheniformis;
KW Bacillus amyloliquefaciens; Bacillus stearothermophilus;
KW Aspergillus oryzae.

OS Aspergillus oryzae.

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XX PN WO9521247-A1.
XX PD 10-AUG-1995.
XX PF 05-OCT-1994; 94WO-DK000371.
XX PR 02-FEB-1994; 94DK-00000141.
XX PA (NOVO ) NOVO-NORDISK AS.
XX PI Toft AH, Marcher D, Pedersen HH, Nilsson TE;
XX WPI; 1995-283767/37.
XX DR
XX PT Use of an oxidation stable alpha-amylase - for simultaneous desizing and
XX bleaching or scouring of fabrics contg. starch or starch derivs.
XX PS Disclosure; Page 25-26; 37pp; English.
XX CC Oxidation stable alpha amylases can be used for the simultaneous desizing
XX and bleaching or scouring of a fabric comprising starch or starch
XX derivatives. They exhibit a better heat stability, especially in the
XX presence of oxidising agents. They are obtained from a parent alpha
XX amylase by replacing one or more methionine residues with any amino acid
XX different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or
XX Asp. The parent alpha amylase is pref. derived from a Bacillus species,
XX although alpha amylases of fungal origin can also be used. This sequence
XX is the wild type (unmodified) alpha amylase of Aspergillus oryzae
XX SQ Sequence 478 AA;
Query Match 78.5%; Score 391; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 ATPADWRSOSIYFLTLTDRPARTDGTATCNTADQKYGCTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSOSIYFLTLTDRPARTDGTATCNTADQKYGCTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTQAOLPQTAYGDVHGYWQDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
Db 61 WITPVTQAOLPQTAYGDVHGYWQDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120
QY 141 NHMGYDGAGSSVDYSVFKEPFSSQDYFHPFCFQNYVEDQTVEDCWLGONTVSLPDLDTTK 200
Db 121 NHMGYDGAGSSVDYSVFKEPFSSQDYFHPFCFQNYVEDQTVEDCWLGONTVSLPDLDTTK 180
QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGNKAAGVYCVGEVLDDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGNKAAGVYCVGEVLDDGDPAYTC 240
QY 261 PYQNVMDGVLYNPIYPLLNAPKSTSGSMDLYNNINTVKSDPCSTLLGTVEVNDNPR 320
Db 241 PYQNVMDGVLYNPIYPLLNAPKSTSGSMDLYNNINTVKSDPCSTLLGTVEVNDNPR 300
QY 321 FASYTNDIALAKNVAFIINDGIPYIYAGQHQHVGAGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAFIINDGIPYIYAGQHQHVGAGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNYAISKDTGFVTYKNWPIYKDD 411
Db 361 LIASANAIRNYAISKDTGFVTYKNWPIYKDD 391
RESULT 4
AAW14500
ID AAW14500 standard; protein; 478 AA.
XX AC AAW14500;
XX XT
XX 04-JUN-1997 (first entry)
XX
```

```
DE Aspergillus oryzae alpha-amylase (mature protein).
XX alpha-amylase; mature; Bacillus licheniformis; termamyl; fungamyl;
XX Aspergillus oryzae; Bacillus amyloliquefaciens; altered property;
KW calcium dependency; substrate binding; stability; pH optimum;
KW thermostability; cleavage; oligosaccharide substrate; dishwashing;
KW washing; detergent additive; fabric desizing; starch liquefaction;
XX sweetener; ethanol production; variant.
XX Aspergillus oryzae.
XX Key Location/Qualifiers
FH Misc-difference 13..45
FT /label= loop 1 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 7-23 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 33"
FT Misc-difference 14..40
FT /label= loop 1 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 8-18 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 35"
FT Misc-difference 28..42
FT /label= loop 1 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 12-19 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 30"
FT Misc-difference 32..38
FT /label= loop 1 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 14-15 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 32"
FT Misc-difference 66..84
FT /label= loop 2 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 44-57 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 18"
FT Misc-difference 70..78
FT /label= loop 2 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 48-51 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 20"
FT Misc-difference 98..210
FT /label= loop 3 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 117-185 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 24"
FT Misc-difference 102..206
FT /label= loop 3 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 121-181 of AAW14499 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 26"
FT Misc-difference 121..181
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to this fragment is deleted or replaced with a fragment
FT corresponding to 102-206 of AAW14499; claim 41"
FT Misc-difference 121..174
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to this fragment is deleted or
```

replaced with a fragment corresponding to 102-199 of AAW14499, claim 42"

Misc-difference 165..1177
/label= loop 3 modification region
/note= "at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 195-202 of AAW14499 is deleted or replaced with a fragment corresponding to this fragment; claim 21"

Misc-difference 166..1173
/label= loop 3 modification region
/note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 196-198 of AAW14499 is deleted or replaced with a fragment corresponding to this fragment; claim 23"

Misc-difference 181..1184
/note= "an amino acid fragment corresponding to this region is deleted from the parent sequence of a variant Fungamyl; claim 43"

Misc-difference 291..313
/label= loop 8 modification region
/note= "at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 322-346 of AAW14498 is deleted or replaced with a fragment corresponding to this fragment; claim 36"

Misc-difference 297..313
/label= loop 8 modification region
/note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 325-345 of AAW14498 is deleted or replaced with a fragment corresponding to this fragment; claim 38"

WO9623874-A1.

08-AUG-1996.

05-FEB-1996; 96WO-DK000057.

03-FEB-1995; 95DK-00000128.

23-OCT-1995; 95DK-00001192.

10-NOV-1995; 95DK-00001256.

(NOVO) NOVO-NORDISK AS.

Svendsen A, Bisgard-Frantzen H, Borchert TV;
WPI; 1996-371424/37.

Alpha-amylase variants and methods of production - have altered properties such as calcium dependency, substrate binding and stability.

Disclosure; Page 87-88; 171pp; English.

The present sequence is the mature Aspergillus oryzae alpha-amylase (A). Variants of parent termamyl- and fungamyl-like alpha-amylases (and methods of constructing them) are claimed. Examples of variants are featured above. The variants have altered properties such as calcium dependency, substrate binding and stability. Also one or more proline or cysteine residues in the variant is modified or replaced with a non-proline or non-cysteine residue such as alanine. The variants can be used for (dish)washing, as detergent additives or for fabric desizing or starch liquefaction. They can also be used for the production of sweeteners and ethanol from starch. See also AAW14498-99

Sequence 478 AA;

Query Match 78 5%; Score 391; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATPADWRSQSIYFLLTDRFARTDGTATCNTADQKYGCGTWQGIIDKLDYIQMGFTAI 60
81 WITPVTALPQTAYGDAYHGYWQDIYSLNENGTADDLKAALSSALHERGMVMDVVA 140
61 WITPVTALPQTAYGDAYHGYWQDIYSLNENGTADDLKAALSSALHERGMVMDVVA 120
141 NHMGVDGAGSDVSVFKPSSQDYFHPFCFIQNYEDQTVEDCWLGDNTVSLPDLDTTK 200
121 NHMGVDGAGSDVSVFKPSSQDYFHPFCFIQNYEDQTVEDCWLGDNTVSLPDLDTTK 180
201 DVKNEWYDWVGSLSVNSYIDGLRIDTVKHVQKDFWPGYNKAAGYVICGEVLDGDPAYTC 260
181 DVKNEWYDWVGSLSVNSYIDGLRIDTVKHVQKDFWPGYNKAAGYVICGEVLDGDPAYTC 240
261 PYQNVMDGVLNYPPIYPLNNAFKSTSGMDDLNNMINTVKSDCPDSTLLGTFVENHDNPR 320
241 PYQNVMDGVLNYPPIYPLNNAFKSTSGMDDLNNMINTVKSDCPDSTLLGTFVENHDNPR 300
321 FASVTNDIALAKNVAAPFIILNDGPIIYAGQEQHVAGGNDPANREATWLSGPTDSELYK 380
301 FASVTNDIALAKNVAAPFIILNDGPIIYAGQEQHVAGGNDPANREATWLSGPTDSELYK 360
381 LIASANAIRNYAISKDTGFVTYKNWPIYKDD 411
361 LIASANAIRNYAISKDTGFVTYKNWPIYKDD 391

RESULT 5
ADT89632
ID ADT89632 standard; protein; 498 AA.
XX
AC ADT89632;
XX
DT 16-DEC-2004 (first entry)
XX
DE Aspergillus niger neutral alpha-amylase A (amyA) protein.
XX
KW Glucoamylase; glaa; amyA; alpha-amylase A; enzyme.
XX
OS Aspergillus niger.
XX
PN US2004191864-A1.
XX
PD 30-SEP-2004.
XX
PF 31-MAR-2004; 2004US-00815495.
XX
PR 31-MAR-2003; 2003US-0459902P.
XX
PA (NOVO) NOVOZYMES BIOTECH INC.
XX
PI Connelly M, Brody H;
XX
DR WPI; 2004-708545/69.
DR N-PSDB; ADT89631.
XX
PT Producing heterologous biological substance comprises culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological substance.
XX
PS Example 11; SEQ ID NO 22; 58pp; English.
XX
CC The present invention relates to a method of producing heterologous biological substance. The method involves culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide sequences comprising modification of glucoamylase (glaA) and recovering heterologous biological substance. the present sequence is the Aspergillus niger neutral alpha-amylase A (amyA) protein.
XX
SQ Sequence 498 AA;

21 ATPADWRSQSIYFLLTDRFARTDGTATCNTADQKYGCGTWQGIIDKLDYIQMGFTAI 80
|||||

Query Match 77.1%; Score 384; DB 8; Length 498;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYAWNSFLYGLQVAAPALAAPADWRSOSIYFLLTDRFARTDGGSTTATCNTADQKYCGG 60
DB 2 MYAWNSFLYGLQVAAPALAAPADWRSOSIYFLLTDRFARTDGGSTTATCNTADQKYCGG 61

QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL 121

QY 121 KALSSALHERGMYLMDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQY 180
DB 122 KALSSALHERGMYLMDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQY 181

QY 181 VEDCWLGDNVTSLPDLDTTKDVVKNEWYDVGSLVSNYSIDGLRIDTVKHVKQDFWPGYN 240
DB 182 VEDCWLGDNVTSLPDLDTTKDVVKNEWYDVGSLVSNYSIDGLRIDTVKHVKQDFWPGYN 241

QY 241 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVNLPIYYPILLNAFKSTSGSMDDLNNMINTVK 300
DB 242 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVNLPIYYPILLNAFKSTSGSMDDLNNMINTVK 301

QY 301 SDPCDSTLLGTFFVENHNDNPRFASNTNDIALAKNVAFAFIILNDGIPPIYAGQBQHYAGND 360
DB 302 SDPCDSTLLGTFFVENHNDNPRFASNTNDIALAKNVAFAFIILNDGIPPIYAGQBQHYAGND 361

QY 361 PANREATWLSGYPTDSELYKLIAS 384
DB 362 PANREATWLSGYPTDSELYKLIAS 385

RESULT 6
ADT89628
ID ADT89628 standard; protein; 499 AA.

AC ADT89628;
XX
DT 16-DEC-2004 (first entry)
XX
DE Aspergillus niger neutral alpha-amylase B (amyB) protein.
XX
KW Glucoamylase; glaA; amyB; alpha-amylase B; enzyme.
XX
OS Aspergillus niger.
XX
PN US2004191864-A1.
XX
PD 30-SEP-2004.
XX
PF 31-MAR-2004; 2004US-00815495.
XX
PR 31-MAR-2003; 2003US-0459902P.
XX
PA (NOVO) NOVOZYMES BIOTECH INC.
XX
PI Connelly M, Brody H;
XX
DR WPI; 2004-708545/69.
DR N-PSDB; ADT89627.
XX
PT Producing heterologous biological substance comprises culturing mutant of
PT wild-type Aspergillus niger strain in medium suitable for producing
PT heterologous biological substance and recovering heterologous biological
PT substance.
XX
XX Example 10; SEQ ID NO 18; 58pp; English.
PS
XX
CC The present invention relates to a method of producing heterologous
CC biological substance. The method involves culturing mutant of wild-type
CC Aspergillus niger strain in medium suitable for producing heterologous

CC biological substance, where mutant strain comprises first nucleotide
CC sequence encoding heterologous biological substance and second nucleotide
CC sequences comprising modification of glucoamylase (glaA) and recovering .
CC heterologous biological substance. The present sequence is the
CC Aspergillus niger neutral alpha-amylase B (amyB) protein.

XX Sequence 499 AA;

Query Match 77.1%; Score 384; DB 8; Length 499;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYAWNSFLYGLQVAAPALAAPADWRSOSIYFLLTDRFARTDGGSTTATCNTADQKYCGG 60
DB 2 MYAWNSFLYGLQVAAPALAAPADWRSOSIYFLLTDRFARTDGGSTTATCNTADQKYCGG 61

QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL 121

QY 121 KALSSALHERGMYLMDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQY 180
DB 122 KALSSALHERGMYLMDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQY 181

QY 181 VEDCWLGDNVTSLPDLDTTKDVVKNEWYDVGSLVSNYSIDGLRIDTVKHVKQDFWPGYN 240
DB 182 VEDCWLGDNVTSLPDLDTTKDVVKNEWYDVGSLVSNYSIDGLRIDTVKHVKQDFWPGYN 241

QY 241 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVNLPIYYPILLNAFKSTSGSMDDLNNMINTVK 300
DB 242 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVNLPIYYPILLNAFKSTSGSMDDLNNMINTVK 301

QY 301 SDPCDSTLLGTFFVENHNDNPRFASNTNDIALAKNVAFAFIILNDGIPPIYAGQBQHYAGND 360
DB 302 SDPCDSTLLGTFFVENHNDNPRFASNTNDIALAKNVAFAFIILNDGIPPIYAGQBQHYAGND 361

QY 361 PANREATWLSGYPTDSELYKLIAS 384
DB 362 PANREATWLSGYPTDSELYKLIAS 385

RESULT 7

ADP96630
ID ABP96630 standard; protein; 1095 AA.

AC ABP96630;

XX
DT 02-JUN-2003 (first entry)

DE Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45.

XX Self-processing plant; plant; processing enzyme; alpha-amylase; grain;
KW pullulanase; alpha-glucosidase; Glucose isomerase; glucoamylase;
KW mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch;
KW maltodextrin; ethanol; fermentation; beverage; enzyme.

XX Aspergillus shirozami.
OS Synthetic.

XX WO2003018766-A2.

XX
PD 06-MAR-2003.

XX 27-AUG-2002; 2002WO-US027129.

XX 27-AUG-2001; 2001US-0315281P.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Lanahan MB, Basu SS, Battie CJ, Chen W, Craig J, Kinkema M;

XX WPI; 2003-268420/26.

DR N-PSDB; ACC44572.

XX Novel polynucleotide encoding hyperthermophilic processing enzymes e.g.
 PT alpha-amylase, useful for producing plant to produce food products having
 PT improved taste or fermentable substrates for ethanol.
 XX
 PS Claim 1; Page 107; 158pp; English.
 XX
 CC The present invention describes polynucleotides which encode processing
 CC enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose
 CC isomerase, or glucoamylase) that are optimised for expression in plants.
 CC The polynucleotides encode mesophilic, thermophilic or hyperthermophilic
 CC processing enzymes, which are activated under suitable conditions to act
 CC upon the desired substrate. Also described are self-processing transgenic
 CC plants and plant parts, e.g. grain, which express one or more of these
 CC enzymes and have an altered composition that facilitates plant and grain
 CC processing. Also described is a method (M) for converting starch to
 CC starch-derived products in a transformed plant part (TPP), by activating
 CC the starch processing enzyme contained in it. Transgenic grain is useful
 CC for preparing maltodextrin. A transformed plant (TP) can be used to
 CC produce food products having improved taste and to produce fermentable
 CC substrates for ethanol and fermented beverages. (M) eliminates the need
 CC to mill or physically disrupt the integrity of plant parts prior to
 CC recovery of starch-derived products. The present sequence represents
 CC alpha-amylase/glucoamylase fusion protein, which is given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 1095 AA;

Query Match 75.7%; Score 377; DB 6; Length 1095;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 21 ATPDWRSGSIYFLTDRPARTDGGTTATCNADQKYGCGTWQGIIDKLDYIQNGFTAI 80
 DB 1 ATPDWRSGSIYFLTDRPARTDGGTTATCNADQKYGCGTWQGIIDKLDYIQNGFTAI 60
 QY 81 WITPVTALPQTAYGDAYHGYYQDDIYSLNENYGTADDKALSSALHERGMYLMDVVA 140
 DB 61 WITPVTALPQTAYGDAYHGYYQDDIYSLNENYGTADDKALSSALHERGMYLMDVVA 120
 QY 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTVEDCWLGDNVTVSLPDLDTTK 200
 DB 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTVEDCWLGDNVTVSLPDLDTTK 180
 QY 201 DVVKNEWDMVGSLSVNSYIDGLRDTVKHQKDFWPGYNKAAGVYCIGEVLDGDPATYC 260
 DB 181 DVVKNEWDMVGSLSVNSYIDGLRDTVKHQKDFWPGYNKAAGVYCIGEVLDGDPATYC 240
 QY 261 PYQNYMDGVLNPIIYYPPLNAPFKSTSGSMDDLNNMINTVKSDCPDSTLLGTFVENHNP 320
 DB 241 PYQNYMDGVLNPIIYYPPLNAPFKSTSGSMDDLNNMINTVKSDCPDSTLLGTFVENHNP 300
 QY 321 FASYTNDIALAKNVAAPFIILNDGIPIIYAGQEQHYAGNDPANREATWLSGYPTDSLYK 380
 DB 301 FASYTNDIALAKNVAAPFIILNDGIPIIYAGQEQHYAGNDPANREATWLSGYPTDSLYK 360
 QY 381 LIASANAIRNVAISKDTGFTVTKNMPYKDDTTIAMRKGTGDSQIVTILSNKGASGDSVT 440
 DB 361 LIASANAIRNVAISKDTGFTVTKNMPYKDDTTIAMRKGTGDSQIVTILSNKGASGDSVT 420
 QY 441 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVFPVPMAGGLPRVLYPTEKLAGSKICSSS 498
 DB 421 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVFPVPMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 8
 AAR79025
 ID AAR79025 standard; protein; 478 AA.
 XX
 AC AAR79025;
 XX
 DT 22-MAR-1996 (first entry)
 XX

DE Mature taka-amylase A.
 XX
 KW Wild type; neopullulanase; B. stearothermophilus; mutant; food industry;
 KW modification; hydrophobicity; replacement insertion; deletion.
 XX
 OS Aspergillus oryzae.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 30. .38
 FT Disulfide-bond 150. .164
 FT Disulfide-bond 240. .283
 FT Disulfide-bond 439. .474
 XX
 PN JP07177891-A.
 XX
 PD 18-JUL-1995.
 XX
 PF 31-OCT-1994; 94JP-00288658.
 XX
 PR 12-NOV-1993; 93JP-00306096.
 XX
 PA (NIDE) NEC CORP.
 PA (EZAK) EZAKI GLICO CO.
 XX
 DR WPI; 1995-279919/37.
 XX
 PT Modifying a transferase by enhancing hydrophobicity of a selected site -
 PT increases transfer activity, also new mutant neo-pullulanase (S).
 XX
 PS Disclosure; Page 10-11; 18pp; English.
 XX
 CC This sequence represents the mature form of taka-amylase from A. oryzae.
 CC This sequence was used in a method for the generation of mutant
 CC pullulanases for use in the food industry (see also AAR79028-28). The
 CC wild type pullulanase enzyme was modified by the method of the invention
 CC for enhancing the hydrophobicity of a selected site of the pullulanase.
 CC The method comprises replacement of a group in the selected site with a
 CC hydrophobic group, replacement of an amino acid with a hydrophobic amino
 CC acid, and/or insertion or deletion of a hydrophobic amino acid from the
 CC selected site. The method was used to produce neopullulanases Y377E,
 CC S422V and M375L
 XX
 SQ Sequence 478 AA;

Query Match 47.8%; Score 238; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 8.5e-219;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 106 DIYSINENYGTADDLKALSSALHERGMYLMDVVDVANHMGYDAGSSVDYSVFKPFSSQDY 165
 DB 86 DIYSINENYGTADDLKALSSALHERGMYLMDVVDVANHMGYDAGSSVDYSVFKPFSSQDY 145
 QY 166 PHPFCFTQNYEDQTVEDCWLGDNVTVSLPDLDTTKDVVKNEWDMVGSLSVNSYIDGLRI 225
 DB 146 PHPFCFTQNYEDQTVEDCWLGDNVTVSLPDLDTTKDVVKNEWDMVGSLSVNSYIDGLRI 205
 QY 226 DTVKHVKQDFWPGYNKAAGVYCIGEVLDGDPATYCPYQNYMDGVLNPIIYYPPLNAPFKST 285
 DB 206 DTVKHVKQDFWPGYNKAAGVYCIGEVLDGDPATYCPYQNYMDGVLNPIIYYPPLNAPFKST 265
 QY 286 SGSMDLLNNMINTVKSDCPDSTLLGTFVENHNPFRFASYYTNDIALAKNVAAPFIILNDG 343
 DB 266 SGSMDLLNNMINTVKSDCPDSTLLGTFVENHNPFRFASYYTNDIALAKNVAAPFIILNDG 323

RESULT 9
 AAR46065
 ID AAR46065 standard; protein; 478 AA.
 XX
 AC AAR46065;
 XX
 DT 25-MAR-2003 (revised)
 DT 18-JUL-1994 (first entry)
 XX

XX DE Mutant alpha-amylase.
 XX KW Methionine substitution; stability; activity; detergent;
 XX KW dishwashing agents; liquefaction agents.
 XX OS Aspergillus oryzae.
 XX WO9402597-A1.
 XX PD 03-FEB-1994.
 XX PF 06-JUL-1993; 93WO-DK000230.
 XX PR 23-JUL-1992; 92DK-00000946.
 XX PR 16-DEC-1992; 92DK-00001503.
 XX PR 15-MAR-1993; 93DK-00000292.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX SVendsen A, Biegard-Prantzen H;
 XX WPI; 1994-048855/06.
 XX PT Mutant alpha-amylase from Bacillus species comprising a methionine
 PT substitution - with improved stability and activity at low pH, for use in
 PT detergents, dishwashing agents and liquefaction agents.
 XX PS Claim 1; Page 7; 20pp; English.
 XX CC The sequence as that of the Aspergillus oryzae alpha amylase, sold
 CC commercially as FUNGAMYL (TM) by Novo Nordisk A/S. The sequence can be
 CC mutated by substitution of one or more of its methionine residues for any
 CC amino acid other than cysteine. The mutant alpha-amylase exhibits a
 CC better activity level and better stability in the presence of oxidising
 CC agents than previous mutant alpha amylases, and improved thermostability
 CC at moderately low pH. The enzyme can be used as an additive for
 CC detergents, dishwashing agents and liquefaction agents. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX SQ Sequence 478 AA;
 Query Match 45.4%; Score 226; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 2.7e-207;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 186 LGDNTVSLPDLDTTKDVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYNKAAGV 245
 DB 166 LGDNTVSLPDLDTTKDVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYNKAAGV 225
 QY 246 YCIGEVLDGDPATCPYQNVMDGVLNPIYYPILLNAFKSTSGSMDDLNNMINTVKSDCPD 305
 DB 226 YCIGEVLDGDPATCPYQNVMDGVLNPIYYPILLNAFKSTSGSMDDLNNMINTVKSDCPD 285
 QY 306 STLLGTFVFNHNDNPRFASVTNDIALKNVAAPFIILNDGPIPIYAGQEQHYAGNDPANRE 365
 DB 286 STLLGTFVFNHNDNPRFASVTNDIALKNVAAPFIILNDGPIPIYAGQEQHYAGNDPANRE 345
 QY 366 ATWLSGYPTDSELYKLIASNAIRNVAISKDTGFTVYKNWPIYKDD 411
 DB 346 ATWLSGYPTDSELYKLIASNAIRNVAISKDTGFTVYKNWPIYKDD 391
 RESULT 10
 ID ABB09072 standard; protein; 423 AA.
 XX ABB09072;
 XX AC ABB09072;
 XX DT 26-JUN-2002 (first entry)
 XX DE Aspergillus oryzae TAKA protein (TAA).
 XX

KW Thermus sp. IM6501; maltogenic amylase; EC 3.2.1.133; crystallisation;
 KW protein co-ordinate data; 3 dimensional structure.
 XX OS Aspergillus oryzae.
 XX PN KR2001027418-A.
 XX PD 06-APR-2001.
 XX PF 09-SEP-1999; 99KR-00039130.
 XX PR 09-SEP-1999; 99KR-00039130.
 XX PA (POST-) POSTECH FOUND.
 XX PA (SAMY-) SAMYANG GENEX CORP.
 XX PI Kim TJ, Park GH;
 XX DR WPI; 2001-534477/59.
 XX PT Manufacturing maltogenic amylase having improved transglycosylation
 PT activity, comprises using crystallization.
 XX PS Disclosure; Page 188; 196pp; Korean.
 XX CC The present invention describes manufacturing maltogenic amylase (EC
 CC 3.2.1.133) having improved transglycosylation activity, comprising using
 CC crystallisation and the three dimensional structure of maltogenic
 CC amylase. Manufacturing maltogenic amylase comprises the following steps:
 CC (i) obtaining a gene of maltogenic amylase from Thermus sp. IM6501 (KCTC
 CC 5027BP) and inserting the gene into plasmid pUC119 to construct
 CC recombinant DNA (pTHMA119); (ii) inserting the recombinant DNA to
 CC Escherichia coli MC1061, which is cultivated at 37 plus degrees Celsius
 CC for 10 hours in Luria-Bertani (LB) media and centrifuging the media to
 CC obtain a microbial cell; (iii) suspending the microbial cell with buffer
 CC solution at pH 7.5 and obtaining supernatant; and (iv) passing the
 CC supernatant through column chromatography and obtaining purified
 CC maltogenic amylase. The maltogenic amylase is a dimer comprised of two
 CC maltogenic amylase molecules, and a Thermus sp. IM6501 maltogenic amylase
 CC (ThMA) crystal. The amylase has a structure containing an activated
 CC region that consists of amino acid residues of Asp-328, Glu-357, Asp-424,
 CC and a pocket with glucose bound that consists of amino acid residues of
 CC Pro44, Tyr45, Arg81, Arg83, Pro118, Cys116, Asn131, Glu132, Val1329,
 CC and His1360. The present sequence represents Aspergillus oryzae TAKA
 CC protein (TAA), given in comparison with ThMA in the present invention
 XX SQ Sequence 423 AA;
 Query Match 14.7%; Score 73; DB 4; Length 423;
 Best Local Similarity 100.0%; Pred. No. 8.9e-61;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 248 IGEVLGGDPATCPYQNVMDGVLNPIYYPILLNAFKSTSGSMDDLNNMINTVKSDCPDST 307
 DB 224 IGEVLGGDPATCPYQNVMDGVLNPIYYPILLNAFKSTSGSMDDLNNMINTVKSDCPDST 283
 QY 308 LLGTFVFNHNDNPR 320
 DB 284 LLGTFVFNHNDNPR 296
 RESULT 11
 ID AAP70311 standard; protein; 46 AA.
 XX AAP70311;
 XX AC AAP70311;
 XX DT 24-OCT-2003 (revised)
 XX DT 25-MAR-2003 (revised)
 XX DT 18-FEB-1991 (first entry)
 XX DE Sequence encoded by the prerregion and the 5' part of the structural gene
 DE for the TAKA-amylase.

```

XX Aspergillus gene expression.
KW Aspergillus oryzae; Hw325.
XX
OS Aspergillus oryzae; Hw325.
XX
XX Key Location/Qualifiers
FH Peptide 1..21
FT Protein 22..46
XX
XX EP238023-A.
XX
XX 23-SEP-1987.
XX
XX 16-MAR-1987; 87EP-00103806.
XX
XX 17-MAR-1986; 86DK-00001226.
XX 17-MAR-1987; 87DK-00001353.
XX
XX (NOVO ) NOVO TERAPEUTISK LAB AS.
XX
XX Boel E, Christensen T, Woeldike HF;
XX
XX WPI; 1987-265414/38.
XX N-PSDB; AAN70507.
XX
XX Expressing proteins, esp. enzymes, in Aspergillus oryzae - by
XX transforming with recombinant vector, pref. contg. the TAKA amylase
XX promoter system.
XX
XX Disclosure; Fig 1; 39pp; English.
XX
XX The patent claims a process for the production of protein products in
XX Aspergillus oryzae and a promoter for use in Aspergillus. The process
XX enables industrial production of many different polypeptides and proteins
XX in A. oryzae. Examples of such products are chymosin or prochymosin and
XX other rennets, proteases, lipases and amylases. (Updated on 25-MAR-2003
XX to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX (Updated on 24-OCT-2003 to standardise OS field)
XX
XX Sequence 46 AA;
XX
XX Query Match 9.0%; Score 45; DB 1; Length 46;
XX Best Local Similarity 100.0%; Pred. No. 7.1e-35;
XX Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MVAWWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGS 45
XX 2 MVAWWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGS 46
XX
XX RESULT 12
XX AAP94631
XX ID AAP94631 standard; protein; 46 AA.
XX
XX AAP94631;
XX
XX 25-MAR-2003 (revised)
XX 01-JUL-1990 (first entry)
XX
XX Aspergillus niger neutral alpha-amylase including prerregion as encoded by
XX plasmids pNA1 and pNA2.
XX
XX Aspergillus niger DSM 2761; neutral alpha-amylase; presequence;
XX plasmid pNA1; plasmid pNA2.
XX
XX Aspergillus niger.
XX
XX Key Location/Qualifiers
XX Peptide 1..21
XX Protein /note="Prerregion"
XX 22..46
XX /note="N-terminal portion"
XX

```

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PN WO8901969-A.
XX
XX 09-MAR-1989.
XX
XX 02-SEP-1988; 88WO-DK000145.
XX
XX 04-SEP-1987; 87DK-00004609.
XX 29-SEP-1987; 87DK-00005126.
XX
XX (NOVO ) NOVO IND AS.
XX
XX Woeldike H;
XX
XX WPI; 1989-085543/11.
XX N-PSDB; AAN91273, AAN91274.
XX
XX Prodn. of proteins in Aspergillus - using promoter and upstream
XX activating sequences derived from Aspergillus niger amylase genes.
XX
XX Fig 2; page 2/11; 38pp; English.
XX
XX The DNA was prepared from mycelium from A. niger DSM 2761. It was
XX screened with a hybridisation probe from TAKA-amylase cDNA and two
XX hybridising clones were found. Plasmids pNA1 and pNA2 each carry the full
XX length amylase gene with promoters and upstream activating sequences.
XX (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
XX correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 46 AA;
XX
XX Query Match 9.0%; Score 45; DB 1; Length 46;
XX Best Local Similarity 100.0%; Pred. No. 7.1e-35;
XX Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MVAWWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGS 45
XX 2 MVAWWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGS 46
XX
XX RESULT 13
XX AAR24437
XX ID AAR24437 standard; protein; 46 AA.
XX
XX AC AAR24437;
XX
XX 24-OCT-2003 (revised)
XX 25-MAR-2003 (revised)
XX 21-NOV-1992 (first entry)
XX
XX Sequence of TAKA-amylase signal and mature protein.
XX
XX Yeast promoter; expression vector; TAKA-amylase; alpha-amylase.
XX
XX Aspergillus oryzae; Hw325.
XX
XX Key Location/Qualifiers
XX Peptide 1..21
XX /label= signal
XX
XX EP489718-A1.
XX
XX 10-JUN-1992.
XX
XX 16-MAR-1987; 92EP-00104421.
XX
XX 17-MAR-1986; 86DK-00001226.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Boel E, Christensen T, Woeldike HF;
XX WPI; 1992-193872/24.
XX N-PSDB; AAQ24569.
XX

```


XX Promoter providing efficient protein prodn. in Aspergillus - is the TAKA
PT amylase promoter, opt. with activating sequences, giving high yields of
PT homologous or heterologous enzymes.

XX Disclosure; Fig 1; 41pp; English.

XX The DNA whose sequence is in AQ24569 was derived from the TAKA- amylase
CC clone. It was inserted in BamHI digested pBR322 to give plasmid pTAKA 17.
CC In pTAKA 17 the A. oryzae derived DNA is shown as a 5.5 kb BamHI/Sau 3AI
CC - BamHI/Sau 3AI fragment, the promoter and upstream activating sequences
CC representing a 2.1 kb fragment. In the method according to the present
CC invention the sequence from nucleotide -1144 to nucleotide -10 has been
CC used as one example of a well functioning part of the promoter region. In
CC another embodiment of the present invention the nucleotide sequence from
CC nucleotide - 1176 to -1 was preceded by the still not sequenced 1.05 kb
CC fragment from pTAKA 17. (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to
CC correct PF field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated
CC on 24-OCT-2003 to standardise OS field)

XX Sequence 46 AA;

Query Match 9.0%; Score 45; DB 2; Length 46;

Best Local Similarity 100.0%; Pred. No. 7.1e-35;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLTLTDRPARTDGS 45

DB 2 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLTLTDRPARTDGS 46

RESULT 14

ABB80177

ID ABB80177 standard; protein; 495 AA.

XX AC ABB80177;

XX 11-AUG-2003 (first entry)

XX A. fumigatus AfAAL1.

XX Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
KW beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
KW polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
KW glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
KW glyceride; starch; maltodextrin; oxidated phenolic compound;
KW polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
KW textile; tea liquor; cleaning ability.

XX Aspergillus fumigatus.

XX WO2003012071-A2.

XX 13-FEB-2003.

XX 05-AUG-2002; 2002WO-US024842.

XX 03-AUG-2001; 2001US-0309870P.

XX (ELIT-) ELITRA PHARM INC.

XX Jiang B, Storms R, Roemer T, Bussey H;

XX WPI; 2003-332729/31.

XX N-PSDB; ABQ80345, ABQ80346.

XX Novel isolated Aspergillus fumigatus polypeptide, useful in various
PT industries such as those involved in the making of food and feed,
PT beverages, textiles and detergents.

XX Claim 17; Page 134-35; 169pp; English.

XX

CC The sequences given in ABB80164-87 show enzymatic proteins derived from
CC A. fumigatus. These proteins display the catalytic activity of an enzyme
CC such as tannase, cellulase, glucose oxidase, glucoamylase, phytase, beta-
CC galactosidase, invertase, lipase, alpha-amylase, laccase,
CC polygalacturonase or xylanase. Compositions comprising the tannase are
CC useful for modulating the amount of compounds that comprise a gallate
CC ester linkage in a composition. Compositions comprising cellulase are
CC useful for modulating the amount of cellulose in a composition.

CC Compositions comprising glucose oxidase are useful for modulating the
CC amount of glucose or oxygen in a composition. Compositions comprising
CC phytase are useful for modulating the amount of myo-inositol phosphates
CC in a composition. Compositions comprising beta-galactosidase are useful
CC for modulating the amount of lactose in a composition. Compositions
CC comprising sucrose or invertase are useful for modulating the amount of
CC sucrose in a composition. Compositions comprising lipase are useful for
CC modulating the amount of glyceride in a composition. Compositions
CC comprising alpha-amylases are useful for modulating the amount of
CC starches or maltodextrins in a composition. Compositions comprising
CC laccase are useful for modulating the amount of oxidated phenolic
CC compounds in a composition. Compositions comprising polygalacturonases
CC are useful for modulating the amount of high or low molecular weight
CC polygalacturonic acid chains in a composition. Compositions comprising
CC xylanases are useful for modulating the amount of xylan or xylo-oligomers
CC in a composition. The A. fumigatus proteins and corresponding DNA's are
CC useful in various industries such as those involved in the making of food
CC and feed, beverages, textiles and detergents. The DNA's are useful to
CC express recombinant enzymes for characterization, modification or
CC industrial uses, to compare with the nucleotide sequence of A. fumigatus
CC to identify duplicated genes of paralogs having the same or similar
CC biochemical activity and/or function, to compare with nucleic acid
CC sequence of other related or distant fungal organisms to identify
CC potential orthologous enzyme genes, for selecting and making oligomers
CC for attachment to a nucleic acid array for examination of expression
CC patterns, and to raise anti-protein antibodies. The polypeptide having
CC tannase activity increases the yield of tea liquor from tea leaves,
CC improves the colour, flavour and health benefits of tea products,
CC particularly an instant tea product. The polypeptide having cellulase
CC activity enhances cleaning ability of detergent compositions

XX Sequence 495 AA;

Query Match 4.6%; Score 23; DB 6; Length 495;

Best Local Similarity 100.0%; Pred. No. 8.2e-13;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 WRSQSIYFLTLTDRPARTDGSITTA 48

DB 25 WRSQSIYFLTLTDRPARTDGSITTA 47

RESULT 15

ADP19639

ID ADP19639 standard; peptide; 20 AA.

XX AC ADP19639;

XX 09-SEP-2004 (first entry)

XX Aspergillus oryzae fungamyl signal peptide sequence.

XX filamentous fungus; signal peptide; fungamyl.

XX Aspergillus oryzae.

XX WO2004050695-A2.

XX 17-JUN-2004.

XX 05-DEC-2003; 2003WO-DK000838.

XX 05-DEC-2002; 2002DK-00001875.

XX (NOVO) NOVOZYMES AS.

XX Hansen TM;
PI
XX
DR WPI; 2004-450719/42.
XX Producing a polypeptide of interest in a filamentous fungus comprises
PT providing a modified DNA sequence by inserting a DNA sequence encoding
PT one or more amino acid residues in between 2 DNA sequences.
XX
XX
PS Disclosure; SEQ ID NO 3; 36pp; English.
XX
XX The invention relates to a method of producing a polypeptide of interest
CC in a filamentous fungus comprising providing a modified DNA sequence by
CC inserting a DNA sequence encoding one or more amino acid residues in
CC between a DNA sequence encoding a polypeptide of interest and the
CC adjacent upstream DNA sequence encoding the N-terminal signal peptide.
CC The methods, DNA sequence, DNA construct and expression vector are useful
CC for producing a polypeptide of interest. This sequence corresponds to the
CC signal peptide sequence from the Aspergillus oryzae fungamyl protein used
CC for producing the polypeptide of interest by the method of the invention.
XX
SQ Sequence 20 AA;
Query Match 4.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVAWWSFLYGLQVAAPALA 20
Db 1 MVAWWSFLYGLQVAAPALA 20

Search completed: November 7, 2005, 19:27:54
Job time : 288.494 secs

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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:25:16 ; Search time 4.09459 Seconds
(without alignments)
661.194 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167

Perfect score: 40

Sequence: 1 SSQDYFH 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003Bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	423	4	ABB09072 Aspergill
2	40	100.0	478	2	Aar46065 Mutant al
3	40	100.0	478	2	Aar72450 Aspergill
4	40	100.0	478	2	Aar78270 Aspergill
5	40	100.0	478	2	Aar79025 Mature ta
6	40	100.0	478	2	Aar14500 Aspergill
7	40	100.0	498	4	Aab84206 Amino aci
8	40	100.0	498	8	Adt89632 Aspergill
9	40	100.0	499	6	Adt89628 Aspergill
10	40	100.0	1095	6	Abp96630 Alpha-amy
11	37	92.5	493	2	Aar88212 Alpha-amy
12	34	85.0	493	4	Aao08447 Human pol
13	34	85.0	1222	3	Aag36453 Arabidops
14	34	85.0	1257	3	Aag36452 Arabidops
15	34	85.0	1275	3	Aag36451 Arabidops
16	33	82.5	116	5	Abp08801 Human ORF
17	33	82.5	124	4	Aao05772 Human pol
18	33	82.5	342	6	Abu70873 Human adi
19	33	82.5	379	8	Ado58298 S. Gomunc
20	33	82.5	2112	7	Adg76988 Human nuc
21	33	82.5	3124	8	Adj78494 EIA bindi
22	33	82.5	4351	7	Adg42622 Rat MEGFI
23	32	80.0	82	8	Adn05042 Antipsori
24	32	80.0	82	8	Adp25302 PRO poly
25	32	80.0	84	8	Adk47501 Streptoco

26	32	80.0	95	8	ADR95807	Adr95807 Novel S.
27	32	80.0	119	5	ABP42992	Abp42992 Human ova
28	32	80.0	180	6	ABU00681	Abu00681 S. pneumo
29	32	80.0	180	6	ADM92084	Adm92084 S. pneumo
30	32	80.0	182	5	ABP28341	Abp28341 Streptoco
31	32	80.0	195	8	ADH45430	Adh45430 Human mol
32	32	80.0	323	6	ABU44715	Abu44715 Protein e
33	32	80.0	326	6	ABP98616	Abp98616 Mature Er
34	32	80.0	348	6	ADP98615	Adp98615 Erwinia c
35	32	80.0	351	8	ADO61605	Ado61605 Transcrip
36	32	80.0	501	4	ABG15126	Abg15126 Novel hum
37	32	80.0	529	4	ABB70891	Abb70891 Drosophil
38	32	80.0	583	2	Aaw26654	Aaw26654 Human PAN
39	32	80.0	583	6	ABG72922	Abg72922 Novel hum
40	32	80.0	583	8	ABM81509	Abm81509 Tumour-as
41	32	80.0	583	3	ADP25358	Adp25358 PRO poly
42	32	80.0	594	3	AAB56501	Aab56501 Human pro
43	32	80.0	685	7	ADK62434	Adk62434 Disease t
44	32	80.0	700	2	AAY33673	Aay33673 B. baasia
45	32	80.0	715	4	AAM79737	Aam79737 Human pro

ALIGNMENTS

RESULT 1
ABB09072
ID ABB09072 standard; protein; 423 AA.

AC ABB09072;

XX 26-JUN-2002 (first entry)

XX Aspergillus oryzae TAKA protein (TAA).

XX Thermus sp. IM6501; maltogenic amylase; EC 3.2.1.133; crystallisation;
XX protein co-ordinate data; 3 dimensional structure.

XX Aspergillus oryzae.

PN KR2001027418-A.

PD 06-APR-2001.

XX 09-SEP-1999; 99KR-00039130.

XX 09-SEP-1999; 99KR-00039130.

XX (POST-) POSTECH FOUND.

PA (SAMY-) SAMYANG GENEX CORP.

XX Kim TJ, Park GH;

XX WPI; 2001-534477/59.

PT Manufacturing maltogenic amylase having improved transglycosylation
PT activity, comprises using crystallization.

PS Disclosure; Page 188; 196pp; Korean.

XX The present invention describes manufacturing maltogenic amylase (EC
3.2.1.133) having improved transglycosylation activity, comprising using
crystallisation and the three dimensional structure of maltogenic
amylase. Manufacturing maltogenic amylase comprises the following steps:
(i) obtaining a gene of maltogenic amylase from Thermus sp. IM6501 (KCTC
5027BP) and inserting the gene into plasmid pUC119 to construct
recombinant DNA (pRhW119); (ii) inserting the recombinant DNA to
Escherichia coli MC1061, which is cultivated at 37 plus degrees Celsius
for 10 hours in Luria-Bertani (LB) media and centrifuging the media to
obtain a microbial cell; (iii) suspending the microbial cell with buffer
solution at pH 7.5 and obtaining supernatant; and (iv) passing the
supernatant through column chromatography and obtaining purified of two
maltogenic amylase. The maltogenic amylase is a dimer comprised of two

CC maltogenic amylase molecules, and a *Thermus* sp. IM6501 maltogenic amylase (ThMA) crystal. The amylase has a structure containing an activated region that consists of amino acid residues of Asp-328, Glu-357, Asp-424, and a pocket with glucose bound that consists of amino acid residues of Pro44, Tyr45, Arg81, Arg83, Pro118, Cys116, Asn1331, Glu1332, Val1329, CC and His1360. The present sequence represents *Aspergillus oryzae* TAKA CC protein (TAA), given in comparison with ThMA in the present invention XX
SQ Sequence 423 AA;

Query Match 100.0%; Score 40; DB 4; Length 423;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 137 SSQDYFH 143

RESULT 2
AAR46065
ID AAR46065 standard; protein; 478 AA.
XX
AC AAR46065;

XX
DT 25-MAR-2003 (revised)
DT 18-JUL-1994 (first entry)

DE Mutant alpha-amylase.

XX Methionine substitution; stability; activity; detergent;
KW dishwashing agents; liquifaction agents.

XX *Aspergillus oryzae*.

XX PN W09402597-A1.

XX PD 03-FEB-1994.

XX PF 06-JUL-1993; 93WO-DK000230.

XX PR 23-JUL-1992; 92DK-00000946.

XX PR 16-DEC-1992; 92DK-00001503.

XX PR 15-MAR-1993; 93DK-00000292.

XX PA (NOVO) NOVO-NORDISK AS.

XX PI Svendsen A, Bisgard-Frantzen H;

XX DR WPI; 1994-048855/06.

PT Mutant alpha-amylase from *Bacillus* species comprising a methionine substitution - with improved stability and activity at low pH, for use in

PT detergents, dishwashing agents and liquifaction agents.

XX Claim 1; Page 7; 20pp; English.

XX The sequence as that of the *Aspergillus oryzae* alpha amylase, sold commercially as FUNGAWYL (TM) by Novo Nordisk A/S. The sequence can be mutated by substitution of one or more of its methionine residues for any amino acid other than cysteine. The mutant alpha-amylase exhibits a better activity level and better stability in the presence of oxidising agents than previous mutant alpha amylases, and improved thermostability at moderately low pH. The enzyme can be used as an additive for detergents, dishwashing agents and liquifaction agents. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 478 AA;

Query Match 100.0%; Score 40; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 3
AAR72450
ID AAR72450 standard; protein; 478 AA.
XX
AC AAR72450;

XX
DT 25-MAR-2003 (revised)
DT 01-DEC-1995 (first entry)

XX *Aspergillus oryzae* alpha amylase (mature protein).

XX Alpha amylase; variant; enzyme; detergent; additive; dishwashing;
KW washing; *Bacillus licheniformis*; *Bacillus amyloliquefaciens*;
KW *Bacillus stearothermophilus*; dyeing; bleaching; scouring; textile;
KW thermostable.

XX *Aspergillus oryzae*.

XX PN W09510603-A1.

XX PD 20-APR-1995.

XX PF 05-OCT-1994; 94WO-DK000370.

XX PR 08-OCT-1993; 93DK-00001133.

XX PR 02-FEB-1994; 94DK-00000140.

XX PA (NOVO) NOVO-NORDISK AS.

XX PI Borchert TV, Bisgard-Frantzen H, Svendsen A, Thellersen M;

XX PI Van Der Zee P;

XX DR WPI; 1995-161790/21.

PT New *Bacillus* derived alpha-amylase variants - having amino acid modifications to improve washing and/or dishwashing performance.

XX Disclosure; Page 75-76; 105pp; English.

XX Variant alpha amylase enzymes which have improved washing and/or as detergent additives. The enzymes have one or more amino acid residues added, deleted or substituted. The variants can also be used for textile desizing prior to scouring, bleaching and dyeing. The variants have improved thermostability, acid/alkaline stability; low temperature optimum; pH optimum; higher hydrolysis velocity and improved tolerance to other composition constituents, e.g. oxidation agents. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 478 AA;

Query Match 100.0%; Score 40; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 4
AAR78270
ID AAR78270 standard; protein; 478 AA.
XX
AC AAR78270;

XX
DT 17-JAN-1996 (first entry)

XX *Aspergillus oryzae* alpha amylase (mature protein).

XX Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch;
 KW thermostable; methionine; Bacillus licheniformis;
 KW Bacillus amyloliquefaciens; Bacillus stearothermophilus;
 KW Aspergillus oryzae.
 OS Aspergillus oryzae.
 XX WO9521247-A1.
 PN 10-AUG-1995.
 XX 05-OCT-1994; 94WO-DK000371.
 XX 02-FEB-1994; 94DK-00000141.
 XX (NOVO) NOVO-NORDISK AS.
 XX Toft AH, Marcher D, Pedersen HH, Nilsson TE;
 XX WPI; 1995-283767/37.
 XX Use of an oxidation stable alpha-amylase - for simultaneous desizing and
 PT bleaching or scouring of fabrics contg. starch or starch derivs.
 XX Disclosure; Page 25-26; 37pp; English.
 XX Oxidation stable alpha amylases can be used for the simultaneous desizing
 CC and bleaching or scouring of a fabric comprising starch or starch
 CC derivatives. They exhibit a better heat stability, especially in the
 CC presence of oxidizing agents. They are obtained from a parent alpha
 CC amylase by replacing one or more methionine residues with any amino acid
 CC different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or
 CC Asp. The parent alpha amylase is pref. derived from a Bacillus species,
 CC although alpha amylases of fungal origin can also be used. This sequence
 CC is the wild type (unmodified) alpha amylase of Aspergillus oryzae
 XX
 XX Sequence 478 AA;
 SQ Query Match 100.0%; Score 40; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SSQDYFH 7
 Db 141 SSQDYFH 147
 RESULT 5
 AAR79025
 ID AAR79025 standard; protein; 478 AA.
 XX AAR79025;
 XX 22-MAR-1996 (first entry)
 DT Mature taka-amylase A.
 DE Wild type; neopullulanase; B. stearothermophilus; mutant; food industry;
 XX modification; hydrophobicity; replacement insertion; deletion.
 KW Aspergillus oryzae.
 OS Key Location/Qualifiers
 FH Disulfide-bond 30..38
 FT Disulfide-bond 150..164
 FT Disulfide-bond 240..283
 FT Disulfide-bond 439..474
 XX JP07177891-A.
 PN 18-JUL-1995.
 PD
 XX

PF 31-OCT-1994; 94JP-00288658.
 XX 12-NOV-1993; 93JP-00306096.
 XX (NIDB) NEC CORP.
 PA (EZAK) EZAKI GLICO CO.
 XX WPI; 1995-279919/37.
 DR Modifying a transferase by enhancing hydrophobicity of a selected site -
 XX increases transfer activity, also new mutant neo-pullulanase(s).
 PT Disclosure; Page 10-11; 18pp; English.
 XX This sequence represents the mature form of taka-amylase from A. oryzae.
 CC This sequence was used in a method for the generation of mutant
 CC pullulanases for use in the food industry (see also AAR79026-28). The
 CC wild type pullulanase enzyme was modified by the method of the invention
 CC for enhancing the hydrophobicity of a selected site of the pullulanase.
 CC The method comprises replacement of a group in the selected site with a
 CC hydrophobic group, replacement of an amino acid with a hydrophobic amino
 CC acid, and/or insertion or deletion of a hydrophobic amino acid from the
 CC selected site. The method was used to produce neopullulanases Y377F,
 CC S422V and M375L
 XX
 XX Sequence 478 AA;
 SQ Query Match 100.0%; Score 40; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SSQDYFH 7
 Db 141 SSQDYFH 147
 RESULT 6
 AAW14500
 ID AAW14500 standard; protein; 478 AA.
 XX AAW14500;
 XX 04-JUN-1997 (first entry)
 DT Aspergillus oryzae alpha-amylase (mature protein).
 DE alpha-amylase; mature; Bacillus licheniformis; termamyl; fungamyl;
 KW Aspergillus oryzae; Bacillus amyloliquefaciens; altered property;
 KW calcium dependency; substrate binding; stability; pH optimum;
 KW thermostability; cleavage; oligosaccharide substrate; dishwashing;
 KW washing; detergent additive; fabric desizing; starch liquefaction;
 KW sweetener; ethanol production; variant.
 XX Aspergillus oryzae.
 OS Key Location/Qualifiers
 FH Misc-difference 13..45
 FT /label= loop 1 modification region
 FT /note= "at least one amino acid residue of a parent alpha
 FT -amylase (used as a template for a variant) corresponding
 FT to 7-23 of AAW14499 is deleted or replaced with a
 FT fragment corresponding to this fragment; claim 33"
 FT Misc-difference 14..40
 FT /label= loop 1 modification region
 FT /note= "preferred region where at least one amino acid
 FT residue of a parent alpha-amylase (used as a template for
 FT a variant) corresponding to 8-18 of AAW14499 is deleted
 FT or replaced with a fragment corresponding to this
 FT fragment; claim 35"
 FT Misc-difference 28..42
 FT /label= loop 1 modification region
 FT /note= "at least one amino acid residue of a parent alpha
 FT -amylase (used as a template for a variant) corresponding

FT to 12-19 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 30"
FT Misc-difference 32. .38
FT /label= loop 1 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 14-15 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 32"
FT Misc-difference 66. .84
FT /label= loop 2 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 44-57 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 18"
FT Misc-difference 70. .78
FT /label= loop 2 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 48-51 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 20"
FT Misc-difference 99. .210
FT /label= loop 3 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 117-185 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 24"
FT Misc-difference 102. .206
FT /label= loop 3 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 121-181 of AAW14499 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 26"
FT Misc-difference 121. .181
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to this fragment is deleted or replaced with a fragment
FT corresponding to 102-206 of AAW14499; claim 41"
FT Misc-difference 121. .174
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to this fragment is deleted or
FT replaced with a fragment corresponding to 102-199 of
FT AAW14499; claim 42"
FT Misc-difference 165. .177
FT /label= loop 3 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 195-202 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 21"
FT Misc-difference 166. .173
FT /label= loop 3 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 196-198 of AAW14499 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 23"
FT Misc-difference 181. .184
FT /note= "an amino acid fragment corresponding to this
FT region is deleted from the parent sequence of a variant
FT Fungamyl; claim 43"
FT Misc-difference 291. .313
FT /label= loop 8 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 322-346 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 36"
FT Misc-difference 297. .313
FT /label= loop 8 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for

FT a variant) corresponding to 325-345 of AAW14498 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 38"
FT XX WO9623974-A1.
FT PN 08-AUG-1996.
FT PD 05-FEB-1996; 96WO-DK000057.
FT PF 03-FEB-1995; 95DK-00000128.
FT PR 23-OCT-1995; 95DK-00001192.
FT PR 10-NOV-1995; 95DK-00001256.
FT XX (NOVO) NOVO-NORDISK AS.
FT PA Svendsen A, Bisgard-Frantzen H, Borchert TV;
FT PI WPI; 1996-371424/37.
FT DR Alpha-amylase variants and methods of production - have altered
FT XX properties such as calcium dependency, substrate binding and stability.
FT PT Disclosure; Page 87-88; 171pp; English.
FT XX The present sequence is the mature Aspergillus oryzae alpha-amylase (A).
FT PS Variants of parent termamyl- and fungamyl-like alpha-amylases (and
FT CC methods of constructing them) are claimed. Examples of variants are
FT CC featured above. The variants have altered properties such as calcium
FT CC dependency, substrate binding and stability. Also one or more proline or
FT CC cysteine residues in the variant is modified or replaced with a non-
FT CC proline or non-cysteine residue such as alanine. The variants can be used
FT CC for (dish)washing, as detergent additives or for fabric desizing or
FT CC starch liquefaction. They can also be used for the production of
FT CC sweeteners and ethanol from starch. See also AAW14498-99
FT XX
FT Sequence 478 AA;
FT Query Match 100.0%; Score 40; DB 2; Length 478;
FT Best Local Similarity 100.0%; Pred. No. 19;
FT Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT QY 1 SSQDYFFH 7
FT |||||
FT Db 141 SSQDYFFH 147
FT
FT RESULT 7
FT AAB84206
FT ID AAB84206 standard; protein; 498 AA.
FT XX
FT AC AAB84206;
FT XX
FT DT 06-AUG-2001 (first entry)
FT XX Amino acid sequence of a fungamyl-like alpha-amylase.
FT DE Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose;
FT XX alcohol; starch; dough improver; brewing; starch liquification.
FT KW
FT XX Aspergillus oryzae.
FT OS
FT PN WO200134784-A1.
FT XX
FT PD 17-MAY-2001.
FT XX
FT PF 10-NOV-2000; 2000WO-DK000626.
FT XX
FT PR 10-NOV-1999; 95DK-00001617.
FT XX (NOVO) NOVOZYMES AS.
FT PA Bisgard-Frantzen H, Svendsen A, Pedersen S;
FT PI

XX WPI: 2001-367478/38.
 DR N-PSDB; AAR90208.
 XX
 PT New variant of Fungamyl-like alpha-amylase, useful for production of
 PT maltose syrups, includes mutations that improve stability against heat
 PT and acidic pH.
 XX
 PS Claim 1; Page 42-45; 49pp; English.
 XX
 CC The present sequence represents a fungamyl-like alpha-amylase. The
 CC specification describes variants of this fungamyl-like alpha-amylase,
 CC which have an alteration in one the amino acid regions 98-110, 150-160,
 CC 161-167, 280-288, 448-455, and 468-475. Each alteration is a deletion or
 CC substitution of an amino acid or an insertion of an amino acid downstream
 CC of a particular position. The variants retain alpha-amylase activity, and
 CC have better heat stability and/or stability at acidic pH, relative to
 CC wild-type enzyme. The variants can therefore be used at higher
 CC temperatures (more efficient conversion or faster reaction, and have
 CC reduced need for cooling and reduced risk of contamination). The variants
 CC may also be used in conjunction with other enzymes, particularly
 CC glucoamylase during dextrinisation. The variants are used to produce
 CC syrups, particularly of high maltose content, or alcohol, from starch; as
 CC dough improver for baked goods; in brewing, to increase fermentability of
 CC the wort; and for liquefaction of starch
 XX
 SQ Sequence 498 AA;

Query Match 100.0%; Score 40; DB 4; Length 498;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||
 DB. 161 SSQDYFH 167

RESULT 8
 ADT89632
 ID ADT89632 standard; protein; 498 AA.

XX AC ADT89632;
 XX DT 16-DEC-2004 (first entry)
 XX DE Aspergillus niger neutral alpha-amylase A (amyA) protein.
 XX KW Glucoamylase; glaA; amyA; alpha-amylase A; enzyme.

XX OS Aspergillus niger.
 XX PN US2004191864-A1.
 XX PD 30-SEP-2004.

XX PF 31-MAR-2004; 2004US-00815495.
 XX PR 31-MAR-2003; 2003US-0459902P.
 XX PA (NOVO) NOVOZYMES BIOTECH INC.

XX PI Connelly M, Brody H;
 XX DR WPI: 2004-708545/69.
 XX DR N-PSDB; ADT89631.

XX PT Producing heterologous biological substance comprises culturing mutant of
 PT wild-type Aspergillus niger strain in medium suitable for producing
 PT heterologous biological substance and recovering heterologous biological
 PT substance.

PS Example 11; SEQ ID NO 22; 58pp; English.

XX

CC The present invention relates to a method of producing heterologous
 CC biological substance. The method involves culturing mutant of wild-type
 CC Aspergillus niger strain in medium suitable for producing heterologous
 CC biological substance, where mutant strain comprises first nucleotide
 CC sequence encoding heterologous biological substance and second nucleotide
 CC sequences comprising modification of glucoamylase (glaA) and recovering
 CC heterologous biological substance. The present sequence is the
 CC Aspergillus niger neutral alpha-amylase A (amyA) protein.
 XX

SQ Sequence 498 AA;

Query Match 100.0%; Score 40; DB 8; Length 498;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||
 DB. 162 SSQDYFH 168

RESULT 9
 ADT89628
 ID ADT89628 standard; protein; 499 AA.

XX AC ADT89628;
 XX DT 16-DEC-2004 (first entry)
 XX DE Aspergillus niger neutral alpha-amylase B (amyB) protein.
 XX KW Glucoamylase; glaA; amyB; alpha-amylase B; enzyme.

XX OS Aspergillus niger.
 XX PN US2004191864-A1.
 XX PD 30-SEP-2004.

XX PF 31-MAR-2004; 2004US-00815495.
 XX PR 31-MAR-2003; 2003US-0459902P.
 XX PA (NOVO) NOVOZYMES BIOTECH INC.

XX PI Connelly M, Brody H;
 XX DR WPI: 2004-708545/69.
 XX DR N-PSDB; ADT89627.

XX PT Producing heterologous biological substance comprises culturing mutant of
 PT wild-type Aspergillus niger strain in medium suitable for producing
 PT heterologous biological substance and recovering heterologous biological
 PT substance.

PS Example 10; SEQ ID NO 18; 58pp; English.

XX
 CC The present invention relates to a method of producing heterologous
 CC biological substance. The method involves culturing mutant of wild-type
 CC Aspergillus niger strain in medium suitable for producing heterologous
 CC biological substance, where mutant strain comprises first nucleotide
 CC sequence encoding heterologous biological substance and second nucleotide
 CC sequences comprising modification of glucoamylase (glaA) and recovering
 CC heterologous biological substance. The present sequence is the
 CC Aspergillus niger neutral alpha-amylase B (amyB) protein.
 XX

SQ Sequence 499 AA;

Query Match 100.0%; Score 40; DB 8; Length 499;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||

```

Db      162 SSQDYFH 168

RESULT 10
ABP96630
ID   ABP96630 standard; protein; 1095 AA.
XX
XX
AC      ABP96630;
XX
DT      02-JUN-2003 (first entry)
XX
XX
DE      Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45.
XX
XX
KW      Self-processing plant; plant; processing enzyme; alpha-amylase; grain;
KW      pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase;
KW      mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch;
KW      maltodextrin; ethanol; fermentation; beverage; enzyme.
XX
XX
OS      Aspergillus shirousami.
OS      Synthetic.
XX
XX      WO2003018766-A2.
XX
XX      06-MAR-2003.
XX
XX      27-AUG-2002; 2002WO-US027129.
XX
XX      27-AUG-2001; 2001US-0315281P.
XX
XX      (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX      Lanahan MB, Basu SS, Battie CJ, Chen W, Craig J, Kinkema M;
XX
XX      WPI; 2003-268420/26.
XX      N-PSDB; ACC44572.
XX
XX      Novel polynucleotide encoding hyperthermophilic processing enzymes e.g.
XX      alpha-amylase, useful for producing plant to produce food products having
XX      improved taste or fermentable substrates for ethanol.
XX
XX      Claim 1; Page 107; 158pp; English.
XX
XX      The present invention describes polynucleotides which encode processing
XX      enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose
XX      isomerase, or glucoamylase) that are optimised for expression in plants.
XX      The polynucleotides encode mesophilic, thermophilic or hyperthermophilic
XX      processing enzymes, which are activated under suitable conditions to act
XX      upon the desired substrate. Also described are self-processing transgenic
XX      plants and plant parts, e.g. grain, which express one or more of these
XX      enzymes and have an altered composition that facilitates plant and grain
XX      processing. Also described is a method (M) for converting starch to
XX      starch-derived products in a transformed plant part (TPP), by activating
XX      the starch processing enzyme contained in it. Transgenic grain is useful
XX      for preparing maltodextrin. A transformed plant (TP) can be used to
XX      produce food products having improved taste and to produce fermentable
XX      substrates for ethanol and fermented beverages. (M) eliminates the need
XX      to mill or physically disrupt the integrity of plant parts prior to
XX      recovery of starch-derived products. The present sequence represents
XX      alpha-amylase/glucoamylase fusion protein, which is given in the
XX      exemplification of the present invention
XX
XX      Sequence 1095 AA;

Query Match      100.0%; Score 40; DB 6; Length 1095;
Best Local Similarity 100.0%; Pred. No. 45;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSQDYFH 7
        |||||
Db      141 SSQDYFH 147

RESULT 11
AAR88212
ID   AAR88212 standard; protein; 493 AA.
XX
XX
AC      AAR88212;
XX
DT      16-OCT-2003 (revised)
DT      03-APR-1996 (first entry)
XX
XX
DE      Alpha-amylase.
XX
XX
KW      Alpha-amylase; thermostable enzyme; baking; Aspergillus niger.
XX
XX
OS      Thermomyces lanuginosus; CBS 224.63.
XX
XX
FH      Key      Location/Qualifiers
FT      Peptide 1..18
FT      /label= Sig_peptide
XX
XX      WO9601323-A1.
XX
XX      18-JAN-1996.
XX
XX      03-JUL-1995; 95WO-EP002607.
XX
XX      04-JUL-1994; 94GB-00013419.
XX
XX      (DANI-) DANISCO AS.
XX
XX      Michelsen B, Rasmussen P;
XX
XX      WPI; 1996-087673/09.
XX      N-PSDB; AAT10562.
XX
XX      Thermophilic alpha-amylase with activity range of 60-80 degrees C -
XX      derived from Thermomyces lanuginosus, useful in the prepn. of foodstuffs
XX      and bakery prods. esp. bread.
XX
XX      Claim 3; Page 36-38; 94pp; English.
XX
XX      A thermostable alpha-amylase (AAR88212) of Thermomyces lanuginosus CBS
XX      224.63 is expressed in Aspergillus niger hosts using a gene (AAT10562)
XX      isolated from a T. lanuginosus gene library. The recombinant enzyme (54-
XX      60 kDa) shows optimal activity at 60-70 deg and pH 5.8-6, has a pI of 3.7
XX      and is active at 60-80 deg. (Updated on 16-OCT-2003 to standardise OS
XX      field)
XX
XX      Sequence 493 AA;

Query Match      92.5%; Score 37; DB 2; Length 493;
Best Local Similarity 85.7%; Pred. No. 76;
Matches      6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSQDYFH 7
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Db      161 NSQDYFH 167

RESULT 12
AAO08447
ID   AAO08447 standard; protein; 52 AA.
XX
XX
AC      AAO08447;
XX
XX
DT      06-NOV-2001 (first entry)
XX
XX
DE      Human polypeptide SEQ ID NO 22339.
XX
XX
KW      Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW      vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW      tissue growth factor; immunomodulatory; cancer; leukaemia;
KW      nervous system disorders; arthritis; inflammation.
XX
XX      Homo sapiens.
OS

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XX WO200164835-A2.
PN
XX
PD
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US004927.
XX
XX
XX 28-FEB-2000; 2000US-00515126.
PR
XX 18-MAY-2000; 2000US-00577409.
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Tang YT, Liu C, Drmanac RT;
PI
XX
XX WPI; 2001-514838/56.
DR
DR N-PSDB; AAI88378.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
XX
PS Claim 20; SEQ ID NO 22339; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 52 AA;
SQ

Query Match 85.0%; Score 34; DB 4; Length 52;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 2 SSQDYMH 8
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RESULT 13
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ID AAG36453 standard; protein; 1222 AA.
XX
XX AAG36453;
AC
XX
XX 18-OCT-2000 (first entry)
DT
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44675.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX
XX EP1033405-A2.
PN
XX
XX 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-00301439.
PF
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XX 25-FEB-1999; 99US-0121825P.
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XX 09-MAR-1999; 99US-0123548P.
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XX 23-MAR-1999; 99US-0125788P.
PR

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PR	05-AUG-1999;	99US-0147260P.	Best Local Similarity 85.7%; Pred. No. 7.5e+02;		
PR	06-AUG-1999;	99US-0147303P.	Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
PR	06-AUG-1999;	99US-0147416P.	QY 1 SSQDYFH 7		
PR	09-AUG-1999;	99US-0147493P.	DB 1130 SSADYFH 1136		
PR	09-AUG-1999;	99US-0147935P.			
PR	10-AUG-1999;	99US-0148171P.	RESULT 14		
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PR	12-AUG-1999;	99US-0148565P.	AC AAG36452;		
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PR	16-AUG-1999;	99US-0149368P.	XX		
PR	17-AUG-1999;	99US-0149175P.	XX		
PR	18-AUG-1999;	99US-0149426P.	XX		
PR	20-AUG-1999;	99US-0149722P.	DT 18-OCT-2000 (first entry)		
PR	20-AUG-1999;	99US-0149723P.	XX		
PR	20-AUG-1999;	99US-0149929P.	XX		
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PR	25-AUG-1999;	99US-0150566P.	KW Protein identification; signal transduction pathway; metabolic pathway;		
PR	26-AUG-1999;	99US-0150884P.	KW hybridisation assay; genetic mapping; gene expression control; promoter;		
PR	27-AUG-1999;	99US-0151065P.	KW termination sequence.		
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Query Match      85.0%; Score 34; DB 3; Length 1257;
Best Local Similarity 85.7%; Pred. No. 7.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 1165 SSADYFH 1171

RESULT 15
AAG36451
ID AAG36451 standard; protein; 1275 AA.
XX
AC AAG36451;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44673.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
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PR 25-FEB-1999; 99US-0121825P.
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PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 85.0%; Score 34; DB 3; Length 1275;

Best Local Similarity 85.7%; Pred. No. 7.9e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSQDYFH 7

Db 1183 SSADYFH 1189

Search completed: November 7, 2005, 18:57:41
Job time : 5.09459 secs

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